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(57) Abstract

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.

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T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF USING SAME

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This invention was made with Government support under Grant Number HL58728 awarded by the National Heart. Lung. and Blood Institute of the National Institutes of Health. The United States Government may have certain rights in this invention.

TECHNICAL FIELD OF THE INVENTION

The present invention relates to cloned T-type calcium channels.

BACKGROUND OF THE INVENTION

Biological membranes are themselves generally impermeable to ionic species. Thus. ions enter cells through regulated pores formed from membrane-associated proteins. Most of these regulated pores are voltage-dependent and are thus able to transduce changes in the transmembrane potential into ion flux. Voltage-gated ion channels form a "superfamily" of related proteins (cf. Jan et al., *Nature. 345*, 672 (1990)). Peculiar to this genus is a high degree of conservation in molecular structure. Generally, voltage-gated channels are membrane bound glycolsylated proteins formed of many subunits. Large α subunits form a pore in the membrane that is selective for a given ionic species. Each α subunit contains four domains (I. II, III. and IV). Each channel domain has six putative transmembrane helical segments (S_1-S_6). In general, the segments within each domain are similar but not identical. Aside from overall structural conservation, certain charged residues within the domains are highly conserved among voltage-gated ion channels (Jan et al., *supra*; Stühmer et al., *Nature. 339*, 597-603 (1989)).

Differences in charged residues between groups of voltage-gated ion channels confer properties unique to each subgroup. such as ion selectivity. For example. most voltage gated ion channels are selective for either sodium, potassium or calcium. Known calcium channels require a ring of negative charge provided by glutamate residues found at similar locations in each of the domains (Yang et al., *Nature. 366*, 158-61 (1993)).

Voltage-gated channels are often classified on the basis of their electrophysiology. The resting membrane potential of most animal cells is between about –70 mV and –80 mV. When the membrane becomes depolarized (moved towards 0 mV), various membrane channels become activated (they are said to

"open"). Thus, one basis for classifying membrane channels is the membrane potential necessary to activate (or "gate") them (voltage dependency). For example, "T-type" calcium channels are activated at a lower voltage than L- or N-type channels (Nowycky et al., *Nature, 316*, 440-43 (1985)). Other physiological properties are the activation kinetics, inactivation kinetics, tail current (deactivation kinetics), and single channel conductance. Thus, in comparison to other calcium currents, T-type calcium current is characteristically short (Chen et al., *J. Gen. Physiol., 96*, 603-30 (1990)), and it exhibits characteristically slow activation kinetics near threshold, fast inactivation kinetics, and slow tail current (Randall et al., *Neuropharmacol., 63*, 879-93 (1997); Carbone et al., *Nature, 310*, 501-02 (1984); Nilius et al., *Nature, 316*, 443-46 (1985)).

Calcium currents have been implicated in many neurological and muscular functions. For example, T-type calcium current is associated with cardiac pacemaker activity, pain transmission in the central nervous system, and in other physiological functions. Defects in T-type calcium current have been implicated in cardiac arrhythmia, hypertension, and epilepsy. Given their potential clinical value, the pharmacological properties of calcium channels have been the subject of extensive study. Most such studies have involved L-type channels because, unlike T-type channels, L-type calcium channels are readily purified from cell extracts. For example, L-type calcium channels have been purified using dihydropyridine drugs (e.g., nifedipine) which can bind with sufficiently high affinity to serve as a ligand for purifying L-type calcium channels. Such purified and cloned L-type calcium channels have been used to develop assays for drugs affecting L-type calcium channels (see, e.g., U.S. Patents 5,429,921 and 5,386,025).

While many electrophysiological characteristics of T-type calcium currents are known, the lack of isolated T-type channels has stalled research into the pharmacology and biophysics underlying the T-type calcium current, at least in comparison with other calcium channels. Indeed, while it is generally assumed that voltage-sensitive ion channels are responsible for the current, no such channel protein, nor any nucleic acid encoding such a protein, has been isolated. In view of the foregoing problems, there exists a need for an isolated T-type calcium channel and a nucleic acid encoding a T-type calcium channel.

BRIEF SUMMARY OF THE INVENTION

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel and cells and cell lines expressing such nucleic acids. The present invention also provides an isolated or substantially purified T-type calcium channel and an isolated or

substantially purified antibody molecule recognizing an epitope on a T-type calcium channel protein.

The present invention is useful for exploring the electrophysiology and pharmacology of the T-type calcium current. Such knowledge can lead to the development of drugs for potentiating or attenuating T-type calcium channels. Thus, the present invention provides an assay for identifying potential drugs affecting T-type calcium channels by exposing cells expressing a T-type calcium channel to a putative drug and then measuring the calcium flux in response to a change in membrane potential. The identification of drugs affecting T-type calcium channels will facilitate even greater understanding of the biophysics of these proteins. Furthermore, some such drugs could have potential clinical applications.

The invention can best be understood with reference to the accompanying drawings and in the following detailed description of the preferred embodiments.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1E compare the complete amino acid sequences of three types of T-type calcium channels (α1G (or Ca_vT.1), α1H (or Ca_vT.2), and α1I (or Ca_vT.3)), indicating conserved functional domains.

Figures 2A-2D are graphic representations of the current-voltage relationships of three cloned T-type calcium channels (Figures 2A, 2B, and 2C) and a cloned R-type calcium channel (Figure 2D).

Figure 3A is a graphic representation of the average current-voltage curve for cloned T-type calcium channels (α1G, triangles, α1H, inverted triangles, α1I, circles), and a cloned R-type calcium channel (filled squares). Figure 3B compares the normalized conductance of a cloned T-type calcium channel at three different concentrations of $BaCl_2$.

Figure 4 depicts average kinetics of the tail current as a function of repolarization potential for α1G (triangles), α1H (inverted triangles), α1I (circles), and a cloned R-type calcium channel (filled squares).

Figures 5A and 5B graphically present data concerning the use of a cloned T-type calcium channel to detect drugs affecting the channel. Figure 6A depicts the effect of 100 µM on current-voltage relationships with a single dosage of miberfradil. Figure 6B illustrates the effect on T-type channel conductance of various doses of miberfradil.

DESCRIPTION OF THE PREFERRED EMBODIMENTS

The present invention provides an isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel α

subunit. The nucleic acid can be of any type, and it can include other elements aside from a sequence encoding a T-type calcium channel domain or domains. For example, where the nucleic acid comprises RNA, it can also include regulatory sequences suitable to permit translation of the RNA. Thus, an RNA nucleic acid of the present invention preferably has at least one ribosome entry site, and preferably has a polyadenosine tail for stabilizing the RNA in the cellular environment. Similarly, DNA nucleic acids of the present invention can have regulatory elements for promoting the transcription of sequence encoding the T-type calcium channel into an RNA such as that described above. For example, a DNA nucleic acid of the present invention can have a promoter and/or an enhancer sequence. While the nucleic acid can be any type of nucleic acid, the nucleic acid preferably comprises a cDNA. A cDNA nucleic acid is preferred over other nucleic acids to permit the nucleic acid to be readily cloned, sequenced, and expressed in a wide variety of cells.

The choice of promoter and/or an enhancer will largely depend on the milieu in which the nucleic acid is to be expressed. Thus, for expression in bacterial cells, the regulatory elements are bacterial promoters. Similarly, for expression in mammalian cells, the regulatory elements are able to effect expression in mammalian cells. While many such regulatory elements are known in the art, examples include prokaryotic promoters and viral promoters (e.g., retroviral ITRs, LTRs, immediate early viral promoters (IEp), such as herpesvirus IEp (e.g., ICP4-IEp and ICP0-IEp), cytomegalovirus (CMV) IEp, and other viral promoters, such as Rous Sarcoma Virus (RSV) promoters, and Murine Leukemia Virus (MLV) promoters). Other suitable promoters are eukaryotic promoters, such as enhancers (e.g., the rabbit β-globin regulatory elements), constitutively active promoters (e.g., the β-actin promoter, etc.), signal specific promoters (e.g., inducible promoters such as a promoter responsive to RU486, etc.), and tissue-specific promoters (e.g., those active in epidermal tissue, dermal tissue, tissue of the digestive organs (e.g., cells of the esophagus, stomach, intestines, colon, etc., or their related glands), smooth muscles, such as vascular smooth muscles, cardiac muscles, skeletal muscles, lung tissue, hepatocytes, lymphocytes, endothelial cells, sclerocytes, kidney cells, glandular cells (e.g., those in the thymus, ovaries, testicles, pancreas, adrenals, pituitary, etc.), tumor cells, cells in connective tissue, cells in the central nervous system (e.g., neurons, neuralgia, etc.), cells in the peripheral nervous system, and other cells of interest).

The isolated or substantially purified nucleic acid of the present invention encodes all or part of a T-type calcium channel α subunit. As used herein, a "calcium channel" includes a protein structure for facilitating the flux of calcium ions across a biological membrane into which the calcium channel is inserted. As used herein, a "T-type channel" is a type of voltage-gated ion channel that facilitates the flux of ions

when the membrane potential of a biological membrane into which it is inserted experiences a slight depolarization. Thus, a T-type calcium channel can begin to gate from about -60 mV to about -30 mV (i.e., about -45 mV to about -35 mV) in about 10 mM Ba^{2+}. Additionally, T-type channels of the present invention exhibit a slow deactivation (tail current) following depolarization. Thus, a T-type calcium channel can exhibit a tail current that decays exponentially with a tau value from about 1 ms to about 10 ms (e.g., from about 4 ms to about 7 ms, such as about 6 ms) following repolarization to a membrane potential from about –80 mV to about –60 mV in a solution with a Ba^{2+} concentration of from about 10 mM to about 40 mM. Another defining characteristic of T-type calcium channels is that they exhibit small single channel conductance. Thus, for example, a T-type channel exhibits a single channel conductance of from about 4 pS to about 12 pS (e.g., from about 6 pS to about 10 pS), and typically from about 7 pS to about 9 pS in a solution with a Ba^{2+} concentration of about 0.1 M.

The isolated or substantially purified nucleic acid of the present invention encodes all or part of any T-type calcium channel having at least one of the aforementioned electrophysiological properties when properly assembled within a cellular membrane. The general structure of calcium channels is summarized above and is otherwise known in the art. Thus, for example, the nucleic acid can encode one of the four functional domains mentioned above. As used herein, a domain of a T-type calcium channel is any protein structure able to associate with three other domains to form a tetrameric body functioning as a T-type calcium channel. While the native T-type calcium channel structure includes all four domains in a single polypeptide (indicated in Figures 1A-1E), a domain can exist as a polypeptide species separate from those containing the other domains. Such separate domains are able to associate within the plasma membrane to form a functional channel. Alternatively, where a plurality of domains are linked within a common polypeptide, the linkage can deviate substantially from the native linkage. Thus, for example, the domains can be linked by polypeptide sequences other than those sequences linking the domains in the native protein (e.g., non-native polyglutamate linkages). Indeed, the domains themselves can include non-native linkages between membrane-spanning elements within the domains. Aside from these modifications, the nucleic acid can encode a chimeric calcium channel domain (or an entire channel) comprising a portion of a T-type calcium channel and a portion derived from another calcium channel (or other channel) protein. For example, the chimera can include portions of domains from T-type channels responsible for low voltage gating and portions of domains from other calcium channels responsible for slow inactivation. Such a protein exhibiting T-type gating but longer inactivation kinetics would facilitate pharmacological research.

As mentioned, nucleic acids of the present invention can encode an entire T-type channel (i.e., a T-type channel protein comprising four functional domains). It has been discovered that at least three genes encoding T-type calcium channels exist in humans and rats (i.e., α1G (or $Ca_vT.1$), α1H (or $Ca_vT.2$), and α1I (or $Ca_vT.3$)), and alternate splicing of these isoforms exist. Examples of the amino acid sequences of full-length T-type channels, and the sequences of suitable coding nucleic acids are set forth at SEQ ID NOs:1-8 (α1G sequences), SEQ IS NOs:9-10 (α1H sequences), and SEQ ID NOs: 11-12 (α1I sequences). However, the invention is not limited to these exemplary sequences. Indeed, as mentioned, an amino acid sequence of a T-type calcium channel can vary from those listed, and it is within the state of the art to change a nucleotide sequence encoding a T-type channel to introduce mutations into the protein. Indeed, for conducting electrophysiological assays, it may be desirable to introduce mutations into such a protein. For example, mutations comprising insertions or deletions can be introduced on either the amino- or carboxy-terminus of the protein, or such mutations can be intrasequence insertions or deletions. Where the electrophysiological properties of the calcium channel are to be conserved, such mutations preferably are in regions other than the membrane spanning domains. However, in some applications (e.g., to decrease inactivation kinetics), the changes can be within the membrane-spanning regions. Moreover, as mentioned above, the sequence can form a protein having only one functional domain of a T-type calcium channel. Additionally, the sequence can also form a chimeric protein or domain, such as those described above.

Aside from insertions and deletion mutations of native T-type calcium channel sequences, a T-type calcium channel can include substitutions of amino acid residues, e.g., for those indicated in SEQ ID NOs:1-12. Preferably, and especially where such a substitution is within a membrane spanning region, the substitution is conservative. Thus, within membrane spanning domains, positively-charged residues (H, K, and R) preferably are only substituted with positively-charged residues; negatively-charged residues (D and E) preferably are only substituted with negatively-charged residues; neutral polar residues (C, G, N, Q, S, T, and Y) preferably are only substituted with neutral polar residues; and neutral non-polar residues (A, F, I, L, M, P, V, and W) preferably are only substituted with neutral non-polar residues. Preferably, any amino-acid substitution within the membrane-spanning regions does not alter this conservation. Most preferably, any substitution, deletion, or insertion does not alter the IVS4 domain. In each of the exemplary T-type calcium channel α subunit sequences, the putative IVS4 region comprises SEQ ID NO:13. Given the strong sequence conservation among families of voltage-gated ion channels, it is likely that this sequence or a derivative sequence, will be present in T-type channels. Thus, the

present invention provides any T-type calcium channel (or a nucleic acid encoding such a T-type calcium channel) comprising SEQ ID NO:13 or a sequence derived from SEQ ID NO:13 having conservative amino acid substitutions. as described above.

The nucleic acid of the present invention encoding all or a part of a T-type calcium channel can be isolated via any suitable method. For example, prior to the present invention, one of skill in the art could design a probe based on the sequence of known. non-T-type, calcium channels and use such probe to screen a genetic library. If such a screen were to identify a putative calcium channel. the researcher could then attempt to clone the entire nucleic acid to characterize it. Similarly, prior to the present invention, to isolate a nucleic acid encoding a T-type calcium channel, one of skill in the art could consult publicly available databases containing DNA sequences (e.g., Genbank) to locate nucleic or amino acid sequences representing a portion of a T-type calcium channel protein or nucleic acid. However. such databases contain no sequence for a full-length T-type calcium channel or identify any sequence as a T-type channel. Such methods assume that T-type calcium channels share sufficient sequence identity with known calcium channel nucleic acids to cross-hybridize, an assumption not supported by any published report. Moreover, prior to the present invention, no partial sequence in such databases was identified as corresponding to a T-type calcium channel. Thus, prior to the present invention, the presence of partial sequences in the public DNA databases could facilitate the isolation of T-type calcium channels only with the exercise of a considerable degree of speculation on the part of the researcher.

By providing several sequences pertaining to T-type calcium channels and a comparison presenting conserved regions and domains, the present invention greatly facilitates the isolation of other nucleic acids encoding T-type calcium channels (or derivatives thereof) with much less experimentation. Thus, while any of the methods discussed above can be employed to isolate other members of this genus, preferably, a nucleic acid encoding a T-type calcium channel is isolated by probing a genetic library using a probe that hybridizes to a DNA encoding a peptide sequence contained in (or similar to) a known T-type calcium channel (e.g., SEQ ID NOs:1-12). To facilitate the isolation of a T-type calcium channel, the present invention provides an isolated polynucleotide hybridizing to a portion of the nucleic acid of the present invention encoding a T-type calcium channel (or a portion thereof). Thus, for example, the present invention includes an isolated polynucleotide hybridizing to SEQ ID NO:1-12. The isolated polynucleotide can hybridize to all or any portion of the sequence encoding the T-type calcium channel.

To isolate such a polynucleotide, any portion of a sequence encoding a T-type calcium channel can be employed as a probe to screen a genetic library, and such screening can be accomplished by standard techniques known in the art. While the probe can hybridize to any portion of such a DNA, preferably the probe is designed to hybridize to a DNA encoding a polypeptide sequence that is highly conserved among T-type calcium channels but is less conserved between the genus of T-type calcium channels and other proteins. Such peptide sequences are readily apparent from the sequence comparison set forth in Figures 1A-1E. Generally, the specificity of hybridization in a genetic screen varies depending on the length of the probe and the stringency (e.g., temperature, salt and detergent concentration, etc.) of hybridization. Stringency of hybridization is broadly classified as "high," "moderate," or "low," and the parameters of these terms are well recognized in the art (see, e.g., Sambrook et al., "Molecular Cloning, a Laboratory Manual," Cold Spring Harbor Press, 1989). The isolated polynucleotide hybridizing to a portion of the nucleic acid encoding a T-type calcium channel can hybridize under any desired stringency conditions. However, for identifying other T-type channels, preferably, the hybridization occurs under moderate stringency, and most preferably under high stringency.

Of course, the isolated or substantially purified polynucleotide can itself be employed as a probe to screen a library as described to isolate a second nucleic acid. In such a screen, one of the polynucleotides will be complementary to a portion of the sequence encoding the T-type calcium channel, and the other isolated nucleic acid will be "sense." Preferably, one of the two isolated polynucleotides (the "sense" strand) itself encodes a T-type calcium channel, or at least one domain thereof. Such a sequence can be cloned to be operably linked to suitable regulatory elements, as described, to produce a T-type calcium channel. Thus, aside from using the nucleic acid of the present invention to produce a T-type calcium channel, the nucleic acids of the present invention are also useful for isolating other sequences encoding T-type calcium channels, or derivatives thereof.

However isolated, the isolated or substantially purified nucleic acid of the present invention is useful, in part, for producing all or a portion of a T-type calcium channel. Thus, the nucleic acid can be introduced into a suitable milieu for driving its expression. Because T-type channels are transmembrane proteins, preferably such a milieu is a living cell. However, it should be understood that the nucleic acid can also be expressed *in vitro* under conditions, such as those known in the art, suitable for *in vitro* transcription and translation. However produced, the present invention includes any protein, such as a recombinant protein or an isolated or substantially purified protein, including all or a portion of a T-type calcium channel or a protein derived from a T-type calcium channel.

For expression in a living cell. the nucleic acid must be introduced into the cell. As nucleic acids are generally introduced into cells as part of genetic vectors, the present invention provides a vector having a T-type calcium channel nucleic acid of the type described above. Any type of vector suitable for introducing the nucleic acid into a host cell is within the context of the present invention. Examples of such vectors include naked DNA and RNA vectors (such as oligonucleotides, plasmids, capped cRNA, etc.), viral vectors such as adeno-associated viral vectors (Berns et al., *Annals of the New York Academy of Sciences, 772*, 95-104 (1995)), adenoviral vectors (Bain et al., *Gene Therapy, 1*, S68 (1994)), herpesvirus vectors (Fink et al., *Ann. Rev. Neurosci., 19*, 265-87 (1996)), packaged amplicons (Federoff et al., *Proc. Nat. Acad. Sci. USA*, 89, 1636-40 (1992)), pappiloma virus vectors, picornavirus vectors, polyoma virus vectors, retroviral vectors, SV40 viral vectors, vaccinia virus vectors, and other vectors. Once a given type of vector is selected, its genome must be manipulated for use as a background vector, after which it must be engineered to incorporate exogenous polynucleotides. Such manipulations are known in the art.

The vectors of the present invention are useful for introducing a nucleic acid encoding all or a portion of a T-type calcium channel into a host cell. Thus, the present invention provides a cell into which the vector of the present invention has been introduced. The host cell can be any cell suitable for expressing the nucleic acid (e.g., bacteria, insect cells, mammalian cells, etc.). The host cell can thus be *in vitro* or *in vivo*. Preferably the cells do not exhibit native T-type calcium current. A preferred cell type is HEK-293 cells because they contain genetic elements that facilitate the expression of transgenes from a variety of expression vectors. For facilitating electrophysiological recordings, oocytes (e.g., *Xenopus* oocytes) are preferred, as they are large and readily handled.

The vector can be introduced into the cell in any manner suitable for the cell type and vector employed. In one embodiment, the vector can be used to prepare an RNA transcript *in vitro* (e.g., a capped cRNA) which is then introduced into the host cell by standard methods (such as injection). Such techniques are preferred when the host cells do not actively transcribe DNA (such as oocytes). In other embodiments, a DNA vector is introduced into the cell such that it is transcribed within the cell. For example, the vector can be introduced into the cell such that it forms an extrachromosomal segment of genetic material in the cell, as is the case with many types of viral vectors. Alternatively, the vector can introduce the nucleic acid into the chromosomal DNA of the host cell.

Preferably, a cell into which the nucleic acid is introduced is also able to express the nucleic acid to produce the α subunit protein. The expression of the nucleic acid can be detected by probing the cell for the presence of T-type calcium

channel mRNA. such as via Northern hybridization analysis. in situ hybridization. etc. More preferably. however. the cell is able to express the nucleic acid to produce the protein including all or a portion of a T-type calcium channel. In such cells. expression of the nucleic acid is confirmed by detecting the protein. for example. by probing cellular extracts with an antibody recognizing the protein (e.g.. on a Western blot. etc.).

In the membrane of the cell producing the protein. the expressed protein contributes to the formation of a functional calcium channel. Where the protein encodes an entire α subunit. the full protein will possess some or all of the electrophysiological properties of T-type calcium channels described above. Where the protein encodes less than an entire channel α subunit (e.g., a domain). the protein will aggregate with other constituent domains in the membrane to form a functional channel. Thus. the presence of the protein can be detected by assaying the cell for T-type calcium channel activity. Indeed. assaying for channel activity serves to determine whether a nucleic acid encoding a putative calcium channel. in fact. encodes a species of T-type channel (as opposed to a member of another genus of calcium channels). For example. when large cells (e.g., oocytes) are used as the host cells, the electrophysiological properties of the channel can be investigated. Thus, the membrane activity of whole cells expressing the nucleic acid can be measured directly. such as via patch clamp techniques using a voltage clamp electrode and a current electrode (Bernal et al., *J. Pharmacol. Exp. Ther.*, *282*, 172-80 (1997)). Alternatively. the activity of single channels can be measured, such as with a standard depolarizing bath and pipette solutions (Lacerda et al.. *Biophys. J.*, *66*, 183-43 (1994)). However measured, the properties of cells into which the putative nucleic acid is introduced are compared to the channel conductance, voltage dependency, activation kinetics, inactivation kinetics, or tail current known for T-type channels and discussed above. A measure of current density (e.g., pA/pF) can also be used to assess the level of gene expression in the cells, normalizing for cellular volume.

While, in accordance with the present invention. an isolated cell into which the T-type calcium channel nucleic acid has been introduced (and preferably stably expressing the nucleic acid to produce the protein) can be prepared, preferably, such transfection protocols result in a population consisting essentially of such transfected cells. For standardizing the results of many experiments, it is even more desirable to employ an established cell line consisting essentially of such cells. Preferably. for use in high throughput assays. cell lines stably expressing a T-type calcium channel exhibit a current density of at least about 40 pA/pF (e.g.. at least about 45 pA/pF). such as about 50 pA/pF or even 55 pA/pF or higher. Preferably. a cell line in accordance with the present invention is able to propagate the nucleic acid through

several passages (e.g.. for at least 10 passages). and. preferably. the nucleic acid is stably integrated into the chromosomes of such cells. Thus. the cell line can propagate the nucleic acid for at least 20 passages, and more preferably significantly more than 20 passages (e.g.. at least about 25 passages. or even more).

Regardless of the cell system, the ability to express a T-type calcium channel nucleic acid within host cells to produce an active channel permits the channel to be further studied. In this regard. the present invention provides a method of identifying a drug which affects T-type calcium channels. The method involves first expressing a T-type calcium channel in a cell to produce an active channel, as herein described. The cell expressing the channel is then exposed to a solution containing a putative drug for interfering with the channel. Thereafter. the presence or absence of calcium flux in response to a change in membrane potential is assayed. Any such assay can be employed within the context of the present invention, (e.g.. using labile dyes, radioisotopes (e.g., ^{45}Ca). recording electrophysiological changes in the membrane, etc.). A quick method of assaying for calcium flux is first to introduce a calcium-sensitive labile dye into the cells. For example, the dye can be one such as those that fluoresce or change color in the presence of calcium, many of which are known to those of skill in the art (e.g., Indo-1). Thereafter, the cells are exposed to a depolarizing solution containing high (e.g., about 50 mM) potassium concentration and a drug, and the reaction of the labile dye is compared to control cells. Using a labile dye affords the ability to assay many putative drugs quickly in a high throughput assay for putative drugs affecting T-type channels. For example, the initial screening can be carried out in 96 well plates. Moreover, dose-response data can be readily generated by exposing the cells to several concentrations of the same putative drug.

Once a putative drug is detected, its effect on the electrophysiology of the cell (e.g.. single channel conductance. voltage dependency, activation kinetics, inactivation kinetics, and tail current of the cells) can be investigated in detail. Generally, the effect of the putative drug on T-type calcium currents is assessed by measuring the various electrophysiological parameters in the presence of various concentrations of the drugs and comparing the data to untreated (or sham-treated) control cells. Cells preferably are maintained in a continuous perfusion chamber during such experiments to facilitate changing solutions. The inventive method of identifying a drug which affects T-type calcium channels can employ any nucleic acid encoding a T-type calcium channel (or derivative thereof). such as those nucleic acids described herein. In fact, as several isoforms of T-type channel exist, the assay method can be repeated using nucleic acids encoding different isoforms to identify

drugs that preferentially target a given isoform. or drugs which affect more than one isoform of T-type calcium channels.

Aside from affording an *in vitro* assay for detecting potential therapeutic or investigative drugs targeting T-type calcium channels. the method of expressing the T-type calcium channel nucleic acid can also be used *in vivo*. For example. as mentioned. several neurological and muscular diseases or disorders have implicated mutations affecting native nucleic acids encoding T-type calcium channels. The present invention. thus, provides a method of treating a disease or disorder associated with a deficiency in a native T-type calcium channel nucleic acid. The method involves introducing a vector having the T-type calcium channel nucleic acid into cells of a host in which native expression of the nucleic acid is deficient. Thus, for example. for treating cardiomyopathy associated with deficiencies in T-type calcium channels, the vector is introduced into myocardial cells. Similarly, for treating forms of epilepsy associated with deficiencies in T-type calcium channels, the vector is introduced into neurons (e.g., thalamic neurons). Within the target cells, the nucleic acid within the vector is expressed to produce active T-type calcium channel. By similar methods, an nucleic acid having a sequence antisense to a sequence encoding a T-type calcium channel (or a portion thereof) can be expressed within a cell. The presence of an antisense sequence can down-regulate the expression of native T-type calcium channel genes by hybridizing to T-type channel mRNA within the cell. Thus, the present invention is useful to treating disorders associated with over-expression of T-type calcium channels.

T-type channel proteins (such as whole T-type calcium channels, domains of such channels, chimeras including portions of T-type calcium channels, etc.) can be employed to generate antibodies (e.g., immunoglobulins) to T-type calcium channels. Thus, the present invention provides an isolated and substantially purified antibody molecule recognizing an epitope on a T-type calcium channel. Such antibodies can be monoclonal antibodies or polyclonal antisera. Antibodies recognizing T-type calcium channels can be used to purify the channels from cell extracts or other solutions by standard methodologies (e.g., immunoprecipitation). Moreover, depending on the location of the epitopes for the antibodies on the T-type calcium channel, the antibodies can be used to affect the channel proteins present on the surface of cells. Thus, antibodies directed to T-type calcium channels are potential reagents for studying the channels as well as for therapy.

Such antibodies can be produced by any suitable method, many of which are well known in the art. Thus, for example, the antibodies can comprise polyclonal antisera obtained from innoculated animals. Alternatively. the antibody molecules can be monoclonal antibodies obtained from a cell line (e.g., a hybridoma cell line). Thus.

the present invention provides a cell which produces such antibodies. Such a cell can be *in vitro* or *in vivo*; however, where the cell is *in vitro*, preferably it is within an established cell line consisting essentially of such cells.

Several examples are presented below to illustrate the invention. Taken together, the examples demonstrate the cloning of twelve novel proteins and their characterization as T-type calcium channel α subunits. These examples are included here for purely illustrative purposes; as such, they are not to be construed so as to limit the scope of any aspect of the invention.

Many procedures employed in the following examples are techniques routinely performed by one of ordinary skill in the art (see generally Sambrook et al., *Molecular Cloning. A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989)) and are not discussed in detail. However, some reagents and methods deserve specific description. Thus, for example, *in vitro* translation and expression were conducted as described previously (Schneider et al., *Receptors and Channels, 2*, 255-70 (1995)). *Xenopus laevis* oocytes were prepared as described previously (Bernal et al., *J. Pharmacol. Exp. Ther., 282*, 172-80 (1997)). To express proteins, 10 or 30 ng of capped cRNA was injected into the oocytes in a volume of 50 nl. For single channel recording, oocytes were injected with 100 ng capped cRNA and incubated for one week prior to assay.

Cells were voltage clamped using a two-microelectrode voltage clamp amplifier as described (Bernal et al., *J. Pharmacol. Exp. Ther., 282*, 172-80 (1997)). The standard bath solution contained the following: 40 mM $Ba(OH)_2$, 50 mM NaOH, 1 mM KOH, 0.1 mM EDTA, and 5 mM HEPES, adjusted to pH 7.4 with methanesulfonate. The osmolality of the 2 mM Ba^{2+} and 10 mM Ba^{2+} solutions was balanced by increasing the NaOH concentration as described (Lory et al., *J. Physiol., (London), 429*, 95-112 (1990)). Voltage and current electrodes (1.5-1.8 M tip resistance) were filled with 3 M KCl. Except as noted, data were acquired at 4 kHz using the pCLAMP system, and filtered at 1 kHz. Data were analyzed using pCLAMP software. Boltzman fits and linear regression were calculated using Prism.

EXAMPLE 1

This example demonstrates the cloning and characterization of putative T-type calcium channels.

A search of the Genbank library was conducted to identify clones identified as having some degree of homology to known calcium channel sequences. The search identified an expressed sequence tagged (EST) partial sequence in a human brain clone (H06096), which was used as a probe to screen a λgt10 cDNA library prepared

from rat brain. Successive screening of the cDNA library identified five overlapping clones which were aligned to construct an entire cDNA sequence, termed α1G.

The α1G cDNA was cloned into the pSP72™ vector and sequenced by standard computer-assisted sequencing. Using the α1G cDNA, the amino acid sequence of the α1G protein was deduced and compared to the sequences of other known calcium channel α subunits. By similar methods, homologous human (H19230 and R19524) and mouse (AA286626) EST clones were also identified and partially sequenced, and alternately spliced variants were identified. The deduced cDNA and amino acid sequences for eight full-length α1G T-type channels are set forth, respectively, as SEQ ID NOs:1-8.

A second T-type calcium channel, termed α1H, was isolated by screening a human heart cDNA library with a fragment of the α1G sequence. An alternately spliced isoform was also identified. The full-length cDNA and amino acid sequences for these α1H T-type channels are set forth, respectively, as SEQ ID NOs:9 and 10.

A third T-type calcium channel, termed α1I, was isolated by screening a rat brain cDNA library at low stringency using a fragment of the rat α1G gene. Fifty plaques were identified, many of which were not detected in a second screening. A third screening with a fragment from α1H identified two clones. Subsequent screening, and the use of the GenBank database, led to the identification of the full length rat and human cDNA and amino acid sequences, set forth at SEQ ID NOs: 11 and 12, respectively.

The α1G, α1H, and α1I amino acid sequences were compared to each other and a known calcium channel (α1E) to investigate the conservation of protein structure and function. The comparison indicates that the α1G, α1H, and α1I amino acid sequences within the putative membrane-spanning domains are about 90 % identical to each other, while the α1G, α1H, and α1I sequences are only roughly 40 % identical to the α1E clone.

Figures 1A-1E indicate this conservation between the proteins. The conservation of charged residues, particularly in the S4 domains, is consistent with the role of the α1G, α1H, and α1I proteins as ion channels. However, two of the glutamates associated with ion specificity in other calcium channels have been replaced with aspartate, suggesting altered ion selectivity. Strikingly, α1G, α1H, and α1I display only low homology to sequences linking the membrane-spanning regions within each domain, and even less homology between the intracellular loops linking domains. Notably, neither α1G, α1H, nor α1I possesses sequences known to bind β subunits or Ca^{2+} ions.

EXAMPLE 2

This example demonstrates the production of cell lines stably expressing the cloned α1G. α1H. and α1I proteins.

HEK-293 cells were transfected with either the rat α1G cDNA (SEQ ID NO:1). the human α1H cDNA (SEQ ID NO:9). or the rat α1I cDNA (SEQ ID NO:11). As a control. cells were also transfected with human α1E plus human β3 (Schneider et al.. *Receptors Channels*, *2*, 255-70 (1994): Murakami et al.. *Eur. J. Biochem.*, *236*, 138-43 (1996)). The DNA constructs included a neomycin resistance gene conferring resistance to G418. The cells were cultured under standard conditions using medium containing G418 to select for stable transformants.

Surviving clones were expanded and assayed for electrophysiological activity to determine the presence of channels within the membrane. Whole-cell currents were recorded from ruptured patches using an Axopatch 200A amplifier. Digidata 1200 A/D converter. and pCLAMP 6.0 software. Data were digitized at 2 kHz and filtered at 1 kHz or off-line. All experiments were performed at room temperature. Pipettes were made out of TW-150-6 capillary tubing (World Precision Instruments. Inc., Sarasota, FL), using a Model P-97 Flaming-Brown pipette puller (Sutter Instrument Co., Novato, CA). The internal pipette solution contained the following: 55 mM CsCl, 75 mM $CsSO_4$, 10 mM $MgCl_2$, 0.1 mM EGTA, 10 mM HEPES, pH adjusted to 7.2 with CsOH. The external Tyrodes solution was the following: 140 mM NaCl, 6 mM KCl, 2 mM $CaCl_2$, 10 mM glucose, 5 mM HEPES, pH 7.4. The recording solution contained the following: 10 mM $BaCl_2$ solution (or 2 mM $CaCl_2$), 140 mM tetraethylammonium (TEA) chloride, 5 mM CsCl. 1 mM $MgCl_2$, 5 mM glucose, and 10 mM HEPES, pH adjusted to 7.4 with TEA-OH. Under these solution conditions the pipette resistance was typically 1.5-2.5 MΩ. Cell capacitance was measured by integrating the charging current during a 10 mV hyperpolarizing pulse (holding potential -80 mV).

Using these recording techniques, values for pA/pF were obtained for each cell line, which is a measure of current density normalizing for cell size. One clone (#N2) expressed the rat α1G protein and has a current density of 42 pA/pF. Another clone (#13), expressed the human α1H protein and exhibited a current density of 53 pA/pF. Three clones (#11, #19, and #25) expressed the rat α1I protein and exhibited current densities of 40 pA/pF, 45 pA/pF, and 55 pA/pF, respectively

EXAMPLE 3

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type current-voltage relationships.

Current traces were elicited by depolarizing voltage clamp pulses of the membranes of cells. The α1G. α1H. and α1I proteins were produced in *Xenopus laevis* oocytes by linearizing the DNA vectors containing the coding sequences. and transcribing the coding sequences *in vitro* by standard methods. Oocytes were then injected with the capped RNA.

Figures 2A-2E depict data obtained from these experiments using cells injected with α1G (Figure 2A). α1H (Figure 2B). and α1I (Figure 2C) and α1E (Figure 2D). These data indicate that cells expressing α1G. α1H. and α1I exhibit T-type calcium current. while oocytes expressing α1E as well as uninjected oocytes (Figure 6A) do not.

Current voltage curves were developed using cells injected with α1G. α1H. α1I. and α1E. Figures 3A depicts such data generated in a 10 mM Ba^{2+} test solution. These data were transformed into conductance and fit with a Boltzman equation to determine the midpoint of activation ($V_{0.5}$). Gating potentials for α1G. α1H. and α1I (-38 ± 1 mV n=8. -44 mV ± 1 mV. n=10. and -31 mV ± 1 mV. n=6. respectively) were in accordance with the gating potential measured for the HEK-293 cells (-41 ± 1 mV, n=10). while α1E required significantly more positive potentials to open (-2.6 mV ± .4 mV, n=3).

To compare the characteristics with published values (Huguenard, *Ann. Rev. Physiol.*, *58*, 329-48 (1996)), the α1G current was recorded at varying concentrations of Ba^{2+}. As indicated in Figure 3B. in solutions containing 2 mM Ba^{2+}, $V_{0.5}$ was -46.5 mV. and the slope factor (k) was 6.6 (n=7). However. when the Ba^{2+} concentration was 40 mM, $V_{0.5}$ was recorded at -21 mV, presumably due to the results of barium on surface charge screening (see, e.g., Wilson et al., *J. Membrane Biol.*, *72*, 117-30 (1983)). Similar values were recorded for α1H and α1I.

These results indicate that α1G, α1H, and α1I are low-voltage activated calcium channels (i.e., from about -60 mV to about -30 mV in 10 mM Ba^{2+}).

EXAMPLE 4

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type tail current.

Tail current was measured at -90 mV after first opening the channels with a voltage step to -10 mV. The voltage-dependence of tail current in cells expressing α1G (oocytes) α1H (HEK 293 cells). and α1I (HEK 293 cells) was measured at varying test potentials. As a control, tail current was also measured from a high voltage activated channel α1E, which Raw data from recordings data were fit with a single exponential and plotted as a function of depolarization potential (Figure 4).

These results demonstrate that the tail currents for the cloned α1G, α1H, and α1I calcium channels are voltage-dependent, consistent with known T-type calcium tail currents. Additionally, these data demonstrate that the tail current for each of the cloned channels is between about 1 ms and about 10 ms following repolarization to a membrane potential from about –80 mV to about –60 mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

EXAMPLE 5

This example demonstrates that the cloned putative T-type calcium channels exhibit T-type single channel conductance.

Measurement of single channel conductance is complicated by the low probability of channel opening at negative potentials when the driving force is large. Thus, single channel conductance was measured similarly for measurements of tail currents to enhance channel opening at negative potentials. Single channels were measured with standard depolarizing bath and pipette (115 mM $BaCl_2$, 1 mM EGTA, and 10 mM HEPES, pH 7.4) solutions (Lacerda et al., *Biophys. J.*, 66, 1833-43 (1994)). Data were analyzed with TRANSIT (VanDongan, *Biophys J.*, 70, 1303-15 (1996)). Single channel amplitudes were measured by averaging the values obtained from Gaussian fits to all-points histograms of traces with openings, selected openings, or amplitude histograms of idealized openings. It has been reported that some oocytes contain a native 9 pS channel. These endogenous channels can be distinguished by their 2-fold larger current amplitudes at the potentials tested (e.g., -20 mV, i = 0.8 for endogenous channels as opposed to 0.4 pA for α1G). However, such endogenous channels were not detected either at the whole cell or single channel level in the oocytes tested.

Current through the main open state of each open channel was measured at each potential and plotted against each test potential. Single channel currents for several patches were then averaged and plotted as a function of test potential, wherein the slope of the plot indicated the single channel conductance. The average slope conductance of the α1G channel was measured at 7.5 ± 1.5 pS, which corresponds with the reported values for T-type calcium channels (Hugenard, *Ann. Rev. Phsysiol.*, *58*, 329-48 (1996)). Similar results were also obtained with both α1H (10.8 ± 1.4 pS). Data collected from recordings of the α1I channels indicate that they open to two distinct amplitudes, The conductance for the small amplitude α1I openings was measured at 3.9 ± 0.5 pS, while that for the large α1I openings was measured at 11.4 ± 0.5 pS).

These results indicate that the cloned α1G, α1H, and α1I proteins exhibit T-type single-channel conductance (e.g., from about 4 to about 12 pS).

EXAMPLE 6

This example demonstrates that a cloned T-type calcium channel can be used for identifying a drug which affects T-type calcium channels.

HEK-293 cells were subjected to treatment as indicated above in Example 3, except that an experimental group of cells were exposed to a solution containing 1 μM mibefradil, a known inhibitor of T-type calcium current. As depicted in Figure 5A, the presence of mibefradil almost completely abolished T-type current in cells expressing α1G. Cells expressing either α1G or α1H were similarly treated using various concentrations of mibefradil to determine a dose-response relationship. These results, depicted in Figure 5B, demonstrate that about 50% inhibition was achieved at a mibefradil concentration of 1 μM.

All of the references cited herein, including patents, patent applications, and publications, are hereby incorporated in their entireties by reference.

While this invention has been described with an emphasis upon preferred embodiments, it will be obvious to those of ordinary skill in the art that variations of the preferred embodiments may be used and that it is intended that the invention may be practiced otherwise than as specifically described herein. Accordingly, this invention includes all modifications encompassed within the spirit and scope of the invention as defined by the following claims.

What is claimed is:

1. A isolated or substantially purified nucleic acid encoding a protein comprising at least one domain of a T-type calcium channel α subunit.

2. The nucleic acid of claim 1, wherein said protein comprises an entire T-type calcium channel α subunit.

3. The nucleic acid of claim 2, wherein said protein comprises SEQ ID NO:13.

4. The nucleic acid of any of claims 1-3, wherein said calcium channel begins to gate from about -60 mV to about -30 mV in 2 mM Ba^{2+}.

5. The nucleic acid of any of claims 1-4, wherein said calcium channel exhibits a tail current of from about 1 ms to about 10 ms following repolarization to a membrane potential from about –80 mV to about –60 mV in a solution with a barium concentration of from about 10 mM to about 40 mM.

6. The nucleic acid of any of claims 1-5, wherein said calcium channel exhibits a single channel conductance of from about 4 pS to about 11 pS in a solution with a barium ion concentration of about 100 mM.

7. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of any of claims 1-6.

8. An isolated or substantially purified nucleic acid hybridizing to the nucleic acid of claim 7.

9. The nucleic acid of claim 8 comprising a sequence encoding at least one domain of a T-type calcium channel α subunit.

10. A vector comprising the nucleic acid of any of claims 1-9.

11. A cell into which the vector of claim 10 has been introduced.

12. The cell of claim 11, which expresses said nucleic acid to produce said protein.

13. The cell of claim 11 or 12, which stably expresses said nucleic acid to produce said protein.

14. A population of cells consisting essentially of cells according to any of claims 11-13.

15. An established cell line consisting essentially of cells according to any of claims 11-13.

16. A method of identifying a drug which affects T-type calcium channels, said method comprising expressing a T-type calcium channel in a cell, exposing said cell to a putative drug, and measuring the calcium flux through the membrane of said cell in response to a change in membrane potential.

17. The method of claim 16, wherein said calcium flux is assayed by using a calcium-sensitive labile dye within said cell.

18. The method of claim 16, wherein said calcium flux is assayed by measuring the electrophysiological properties of said cell.

19. The method of claim 16, wherein said calcium channel comprises SEQ ID NO:13.

20. An isolated or substantially purified immunoglobulin recognizing an epitope on a T-type calcium channel protein.

21. A cell *in vitro* which produces the immunoglobulin of claim 20.

22. An established cell line consisting essentially of cells according to claim 21.

```
hCavT1a MDEEEDGAGAEESGQPR------------------SFMRLNDLSGAGGRPGPGSAEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPW
rCavT1a MDEEEDGAGAEESGQPR------------------SFTQLNDLSGAGGRQGPGSTEKDPGSADSEAEGLPYPALAPVVFFYLSQDSRPRSWCLRTVCNPW
hCavT2a MTEGARAADEVRVPLGRRPWPCGVGGVPGEPRGAGTRGGGGFELGVSPSESPAAERCAELGADEEQRVPYPALAATVFFCLGQTTRPRSWCLRLVCNPW
hCavT3  MAESASPPSSSAAA--------------------PAAEPGVTTEQPGPRSPPSSPPGLEEPLDGADPHVPHPDLAPIAFFCLRQTTSPRNWCIKMVCNPW
rCavT3  MADSNLPPSSAAAP-------------------APEPG--ITEQPGPRSPPPSPPGLEEPLEGTNPDVPHPDLAPVAFFCLRQTTSPRNWCIKMVCNPW

             IS1                                   IS2                          IS3
hCavT1a FERISMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTV
rCavT1a FERVSMLVILLNCVTLGMFRPCEDIACDSQRCRILQAFDDFIFAFFAVEMVVKMVALGIFGKKCYLGDTWNRLDFFIVIAGMLEYSLDLQNVSFSAVRTV
hCavT2a FEHVSMLVIMLNCVTLGMFRPCEDVECGSERCNILEAFDAFIFAFFAVEMVIKMVALGLFGQKCYLGDTWNRLDFFIVVAGMMEYSLDGHNVSLSAIRTV
hCavT3  FECVSMLVILLNCVTLGMYQPCDDMDCLSDRCKIMQVFDDFIFIFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTV
rCavT3  FECVSMLVILLNCVTLGMYQPCDDMECLSDRCKILQVFDDFIFIFFAMEMVLKMVALGIFGKKCYLGDTWNRLDFFIVMAGMVEYSLDLQNINLSAIRTV

          IS4                      IS5
hCavT1a RVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVD-LERYYQTENEDESPFICSQPRENGMRS
rCavT1a RVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLPENFSLPLSVD-LEPYYQTENEDESPFICSQPRENGMRS
hCavT2a RVLRPLRAINRVPSMRILVTLLLDTLPMLGNVLLLCFFVFFIFGIVGVQLWAGLLRNRCFLDSAFVRNNNLTFLRPYYQTEEGEENPFICSSRRDNGMQK
hCavT3  RVLRPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVA-LPPYYQPEEDDEMPFICSLSGDNGIMG
rCavT3  RVLRPLKAINRVPSMRILVNLLLDTLPMLGNVLLLCFFVFFIFGIIGVQLWAGLLRNRCFLEENFTIQGDVA-LPPYYQPEEDDEMPFICSLTGDNGIMG

                                                                              IP LOOP
hCavT1a CRSVPTLRGDG-----GGGPPCGLDYEAYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFI
rCavT1a CRSVPTLRGEG-----GGGPPCSLDYETYNSSSNTTCVNWNQYYTNCSAGEHNPFKGAINFDNIGYAWIAIFQVITLEGWVDIMYFVMDAHSFYNFIYFI
hCavT2a CSHIPGRRDVRMPCTLGWEA-YTQPQAEGVGAARNACINWNQYYNVCRSGDSNPHNGAINFDNTCYAWIAIFQVITLEGWVDIMYYVMDAHSFYNFIYFI
hCavT3  CHEIPPLKEQGRECCLSKDDVYDFGAGRQDLNASGLCVNWNRYYNVCRTGSANPHKGAINFDNIGYAWIVIFQVITLEGWVEIMYYVMDAHSFYNFIYFI
rCavT3  CHEIPPLKEQGRECCLSKDDVYDFGAGRQDLNASGLCVNWNRYYNVCRTGNANPHKGAINFDNIGYAGIVIFQVITLEGWVEIMYYVMDAHSFYNFIYFI

           IS6
hCavT1a LLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAAGVRVGLLSSPAPLGGQET
rCavT1a LLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRVRFLSNASTLASFSEPGSCYEELLKYLVYILRKAARRLAQVSRAIGVRAGLLSSPVARSGQEP
hCavT2a LLIIVGSFFMINLCLVVIATQFSETKQRESQLMREQRARHLSNDSTLASFSEPGSCYEELLKYVGHIFRKVKRRSLRLYARWQSRWRKKVDPSAVQGQGP
hCavT3  LLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLSS-STVASYAEPGDCYEEIFQYVCHILRKAKRRALGLYQALQSRRQ-------------
rCavT3  LLIIVGSFFMINLCLVVIATQFSETKQREHRLMLEQRQRYLSS-STVASYAEPGDCYEEIFQYVCHILRKAKRRALGLYQALQNRRQ-------------
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Fig. 1A

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hCavT1a QPSSSCSRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRAPRASPEIQDRDANGSRRLMLPPPSTPALSGAPPGGA--------ESVHSFYHADCHLEPVRC
rCavT1a QPSGSCTRSHRRLSVHHLVHHHHHHHHHYHLGNGTLRVPRASPEIQDRDANGSRRLMLPPPSTPTPSGGPPRGA--------ESVHSFYHADCHLEPVRC
hCavT2a GHRQRRAGRHTASVHHLVYHHHHHHHHHYHFSHGSPRRPGPEPGACDTRLVRAGAPPSPPSPGRGPPDAESVHSIYHADCHIEGPQERARVGTCRSHCRC
hCavT3  ----------------------------------------------------------------------------------------------------
rCavT3  ----------------------------------------------------------------------------------------------------

hCavT1a QAPPPRSPSEASGRTVGSGKVYPTVHTSPPPETLKEKALVEVAASSGPPTLTSLN-IPPGPYSSMHKLLETQSTGACQSSCKISSPCLKADSGACGPDSC
rCavT1a QAPPPRCPSEASGRTVGSGKVYPTVHTSPPPEILKDKALVEVAPSPGPPTLTSFN-IPPGPFSSMHKLLETQSTGACHSSCKISSPCSKADSGACGPDSC
hCavT2a QPQAGHRAGHHELPHDPALRGGQRQRQHQPRTQGEVGRWTARHRGHGPLSLNSPDPYEKIPHVAGEHGLGQAPGHLSGLSVPCPLPSPPAGTLTCELKSC
hCavT3  ---------------------------------------------ALGPEAPAPAKPGPHAKEPRHYQLCPQHSPLDATPHTLVQPIPATLASDPASC
rCavT3  ---------------------------------------------AMGPGTPAPAKPGPHAKEPSHCKLCPRHSPLDPTPHTLVQPISAILASDPSSC

hCavT1a PYCARA-GAGEVELADREMPDSDSEAVYEFTQDAQHSDLRDPHS---------------RR-QRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIM
rCavT1a PYCART-GAGEPESADHVMPDSDSEAVYEFTQDAQHSDLRDPHS---------------RRRQRSLGPDAEPSSVLAFWRLICDTFRKIVDSKYFGRGIM
hCavT2a PYCTRALEDPEGELSGSESGDSDGRGVYEFTQDVRHGDRWDPTRPPRATDTPGPGPGSPQRRAQQRAAPGEPGWMGRLWVTFSGKLRRIVDSKYFSRGIM
hCavT3  PCCQHEDGRRPSGLGSTDSGQEGS------GSGSSAGGEDEADGDGARSSEDGASSELGKEEEEEEQADGAVWLCGDVWRETRAKLRGIVDSKYFNRGIM
rCavT3  PHCQHEAGRRPSGLGSTDSGQEGS------GSGGSA--EAEANGDGLQSSEDGVSSDLGKEEEQE---DGAARLCGDVWRETRKKLRGIVDSKYFNRGIM

         IIS1                              IIS2                             IIS3                       IIS4
hCavT1a IAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPA
rCavT1a IAILVNTLSMGIEYHEQPEELTNALEISNIVFTSLFALEMLLKLLVYGPFGYIKNPYNIFDGVIVVISVWEIVGQQGGGLSVLRTFRLMRVLKLVRFLPA
hCavT2a MAILVNTLSMGVEYHEQPEELTNALEISNIVFTSMFALEMLLKLLACGPLGYIRNPYNIFDGIIVVISVWEIVGQADGGLSVLRTFRLLRVLKLVRFLPA
hCavT3  MAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLKLVRFMPA
rCavT3  MAILVNTVSMGIEHHEQPEELTNILEICNVVFTSMFALEMILKLAAFGLFDYLRNPYNIFDSIIVIISIWEIVGQADGGLSVLRTFRLLRVLKLVRFMPA

                             IIS5                                       IIP LOOP
hCavT1a LQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMT
rCavT1a LQRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHLFGCKFASERD-GDTLPDRKNFDSLLWAIVTVFQILTQEDWNKVLYNGMASTSSWAALYFIALMT
hCavT2a LRRQLVVLVKTMDNVATFCTLLMLFIFIFSILGMHLFGCKFSLKTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSSWAALYFVALMT
hCavT3  LRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTSPWASLYFVALMT
rCavT3  LRRQLVVLMKTMDNVATFCMLLMLFIFIFSILGMHIFGCKFSLRTDTGDTVPDRKNFDSLLWAIVTVFQILTQEDWNVVLYNGMASTTPWASLYFVALMT
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Fig. 1B

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          IIS6
hCavT1a FGNYVLFNLLVAILVEGFQAEGDANKSESEPDFFSPSLDGDGDRKKCLALVSLGEHPELRKSLLPPL-----IIHTAATPMSLPKSTSTGLGEALGPASR
rCavT1a FGNYVLFNLLVAILVEGFQAEGDATKSESEPDFFSPSVDGDGDRKKRLALVALGEHAELRKSLLPPL-----IIHTAATPMSHPKSSSTGVGEALGSGSR
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```

Fig. 1C

```
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                                                            IVS1                           IVS2
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hCavT2a RRREEKRLRRLERRRR-STFPSPEAQRRPYYADYSPTRRWIHSLCTSHYLDLFITFIICVNVITMSMEHYNQPKSLDEALKYCNYVFTIVFVFEAALKLV
hCavT3  RRREEKRLRRLEKKRR-K------AQRLPYYATYCHTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKLV
rCavT3  RRREEKRLRRLEKKRR-K------AQRLPYYATYCPTRLLIHSMCTSHYLDIFITFIICLNVVTMSLEHYNQPTSLETALKYCNYMFTTVFVLEAVLKLV

                IVS3                          IVS4                               IVS5
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rCavT3  AFGLRRFFKDRWNQLDLAIVLLSVMGITLEEIEINAALPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLFMLLFFIYAALGVE

                           IVP LOOP                                        IVS6
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hCavT3  AQEDAEMDAELELEMAHGLGP-------------------------------------------------------------------------------
rCavT3  AQEDAEMDAEIELEMAHGLGPCPGPCPGPCPCPCPCPCA-------------------------------------------------------------
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Fig. 1D

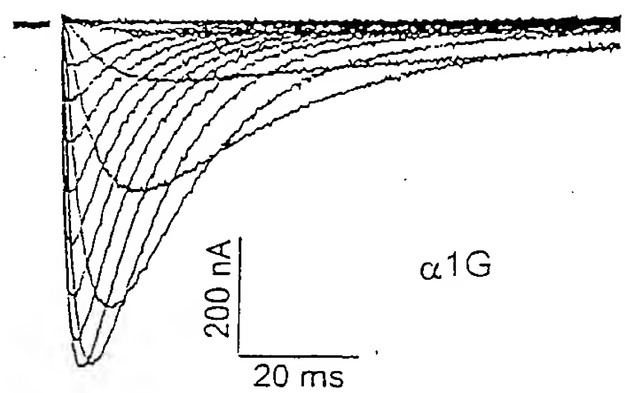
hCa$_v$T1a SYMCRHGSTAEGPLGHRGWGLPKAQSGSVLSVHSQPADTSYILQLPKDAPHLLQPHSAPTWGTIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRE
rCa$_v$T1a SYMCRNGSTAERSLGHRGWGLPKAQSGSILSVHSQPADTSCILQLPKDVHYLLQPHGAPTWGAIPKLPPPGRSPLAQRPLRRQAAIRTDSLDVQGLGSRE
hCa$_v$T2a SYMFRPVVPASAPHPRPLQEVEMETYGAGTPLGSVASVHSPPAESCASLQIPLAVSSPARSGE-------------------------------------
hCa$_v$T3 ----------GPRLPTGSPGAPGRGPGGAGGGGDTDGGLCRRCYSPAQENLWLDSVSLIIKDS-------------------------------------
rCa$_v$T3 ----------GPRLPTSSPGAPGRGSGGAGAGGDTESHLCRHCYSPAQETLWLDSVSLIIKDS-------------------------------------

hCa$_v$T1a DLLAEVSGPSPPLARAYSFWGQSSTQAQQHSRSHSKISKHMTPPAPCPGPEPNWGKGPPETRSSLELDTELSWISGDLLPPGGQEEPPSPRDLKKCYSVE
rCa$_v$T1a DLLSEVSGPSCPLTRSSSFWGGSSIQVQQRSGIQSKVSKHIRLPAPCPGLEPSWAKDPPETRSSLELDTELSWISGDLLPSS-QEEPLFPRDLKKCYSVE
hCa$_v$T2a ------------PLHALSPRGTARSPSLSRLLCRQEAVHTDSLKGRLTALGTPWILQSLVRKPR (SEQ ID NO:9)
hCa$_v$T3 ------------LEGELTIIDNLSGSIFHHYSSPAGCKKCHHDKQETGPRPSCWVTT (SEQ ID NO:11)
rCa$_v$T3 ------------LEGELTIIDNLSGSVFHHYASPDGCGKCHHDKQETGLHPSCWGMT (SEQ ID NO:12)

hCa$_v$T1a AQSCQRRPTSWLDEQRRHSIAVSCLDSGSQPHLGTDPSNLGGQPLGGPGSRPKKKLSPPSITIDPPESQGPRTPPSPGICLRRRAPSSDSKDPLASGPPD
rCa$_v$T1a TQSCRRRPGFWLDEQRRHSIAVSCLDSGSQPRLCPSPSSLGGQPLGGPGSRPKKKLSPPSISIDPPESQGSRPPCSPGVCLRRRAPASDSKDPSVSSPLD

hCa$_v$T1a SMAASPSPKKDVLSLSGLSSDPADLDP (SEQ ID NO:1)
rCa$_v$T1a STAASPSPKKDTLSLSGLSSDPTDMDP (SEQ ID NO:5)

Fig. 1E



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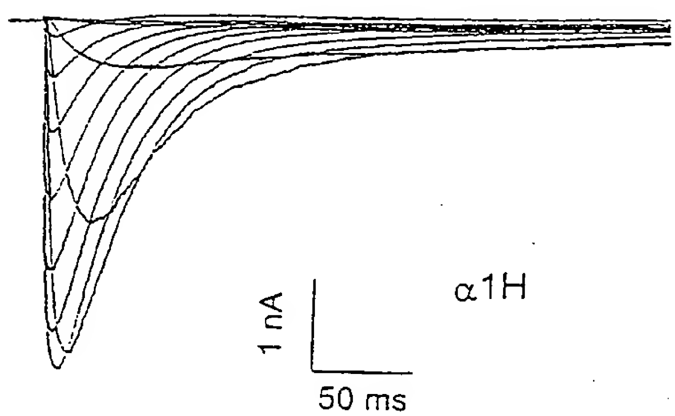

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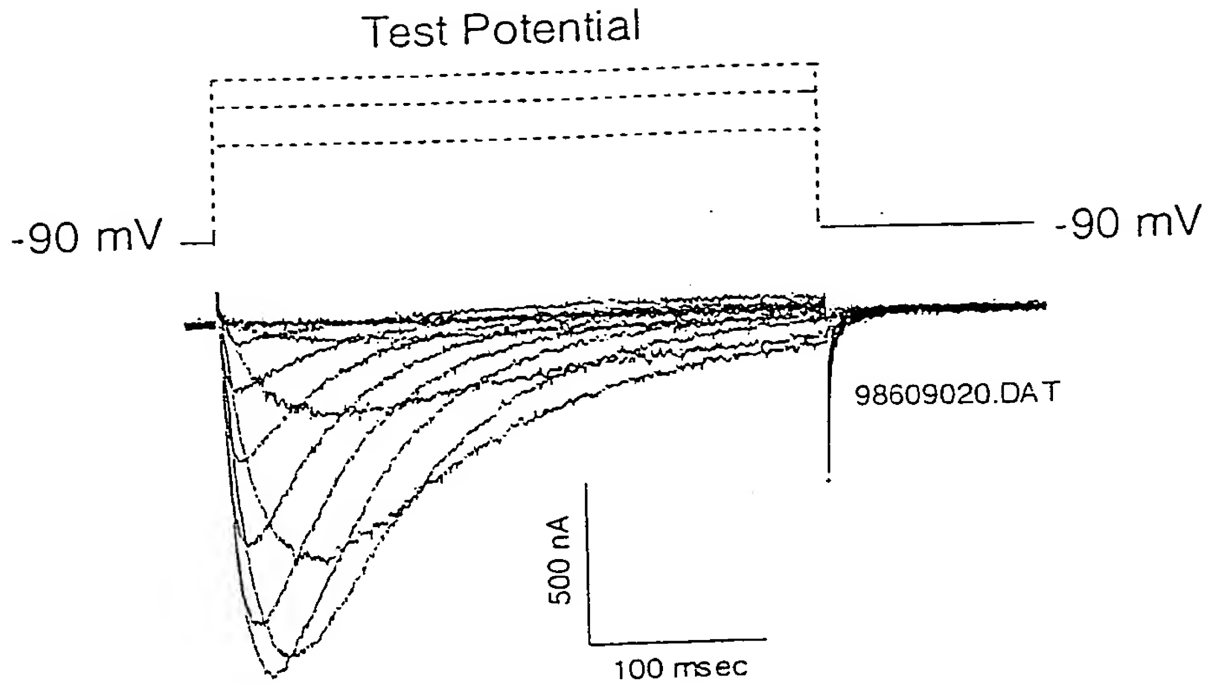

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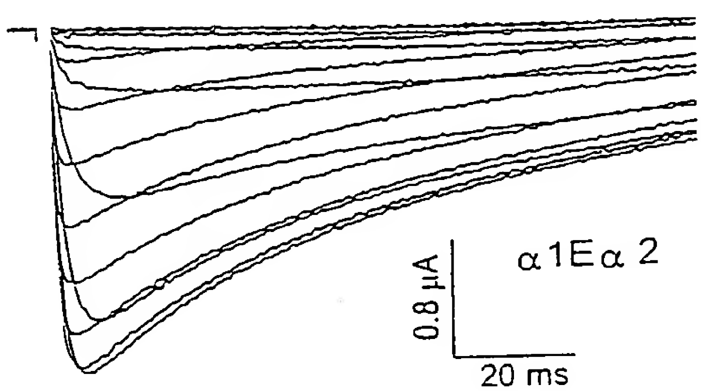

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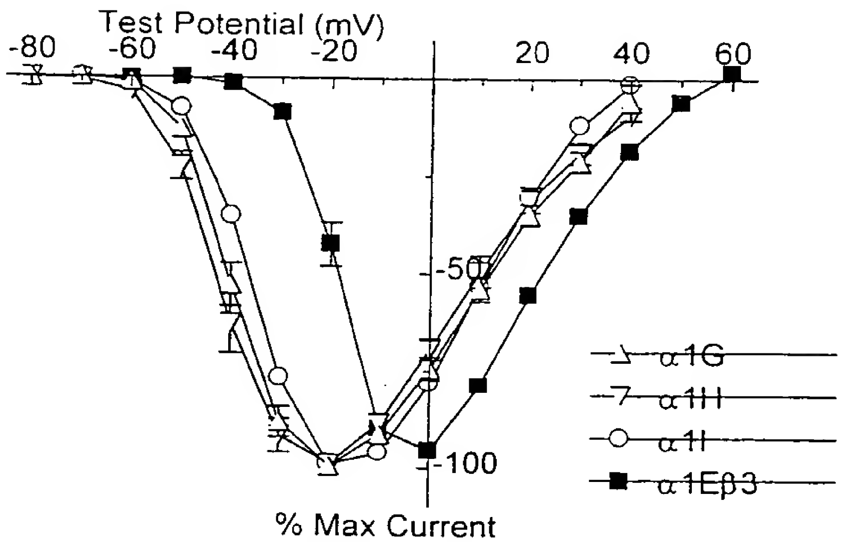

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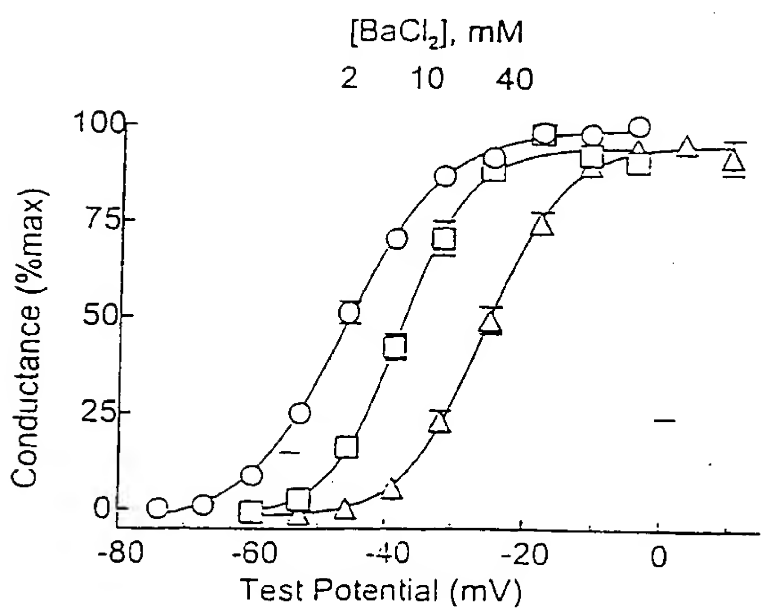

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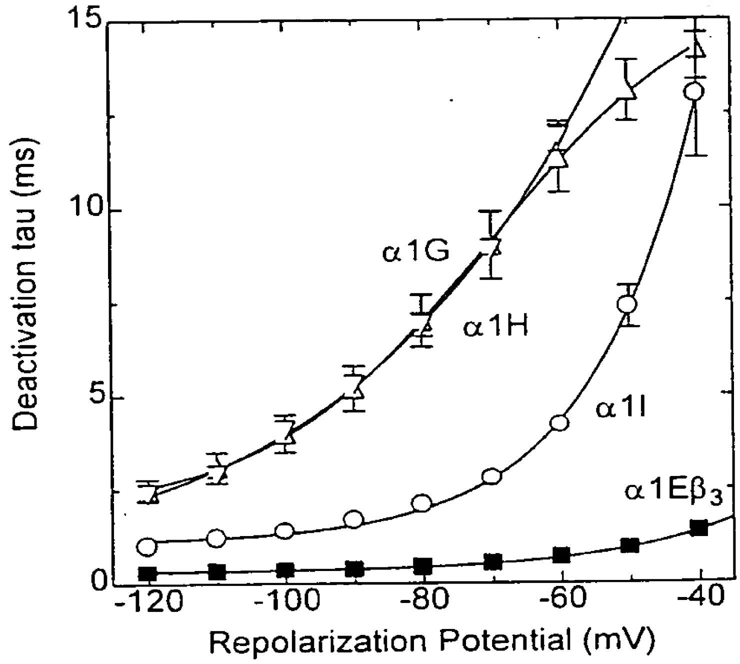
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10
5
0
Deactivation tau (ms)
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α1H
α1I
α1Eβ3
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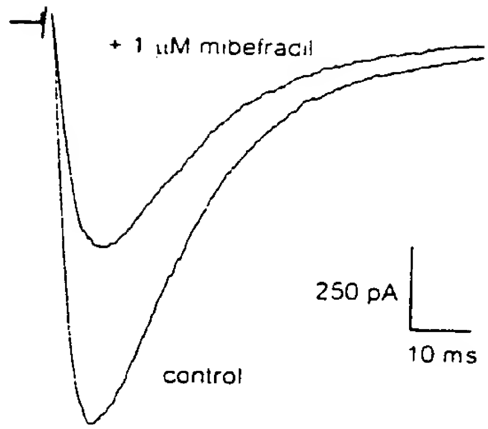
-100
-80
-60
-40
Repolarization Potential (mV)

Figure 4



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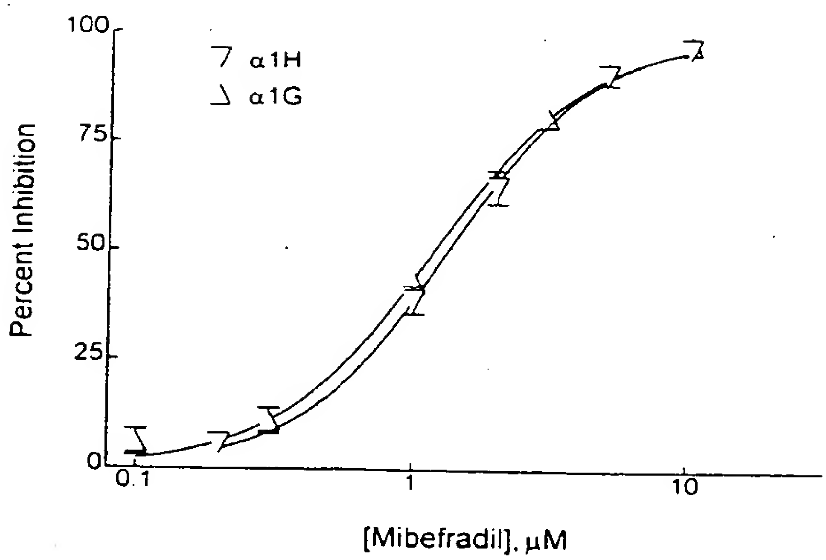

Figure 5B

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      Cribbs, Leanne L.
      Loyola University of Chicago

<120> T-TYPE VOLTAGE-GATED CALCIUM CHANNELS AND METHOD OF
      USING SAME

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<150> US 08/985,809
<151> 1997-12-05

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Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
             20                  25                  30

ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg     144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
         35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg     192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
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ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg     288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
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acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag     336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
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Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
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Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
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tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac     576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
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Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
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755 760 765

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Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
770 775 780

ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt 2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785 790 795 800

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc 2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
805 810 815

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg 2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
820 825 830

ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg 2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
835 840 845

ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac 2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
850 855 860

gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc 2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865 870 875 880

atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat 2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
885 890 895

ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc 2736

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Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
                900                 905                 910

atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc    2784
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
            915                 920                 925

ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc    2832
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
    930                 935                 940

att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc    2880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945                 950                 955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc    2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                 970                 975

gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac    2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                 985                 990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg    3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
        995                 1000                1005

cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc    3072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                1015                1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc    3120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                1030                1035                1040

cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg    3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                1045                1050                1055

gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc    3216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060                1065                1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac    3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
        1075                1080                1085

agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag    3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
    1090                1095                1100

cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag    3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105                1110                1115                1120

gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc    3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                1125                1130                1135

cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca    3456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140                1145                1150

gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg    3504
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Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
1155 1160 1165

tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc 3552
Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
1170 1175 1180

ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac 3600
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185 1190 1195 1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg 3648
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
1205 1210 1215

atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca 3696
Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
1220 1225 1230

gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg 3744
Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
1235 1240 1245

atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc 3792
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
1250 1255 1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac 3840
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
1265 1270 1275 1280

agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca 3888
Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
1285 1290 1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc 3936
Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
1300 1305 1310

ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg 3984
Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
1315 1320 1325

ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct 4032
Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
1330 1335 1340

gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg 4080
Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
1345 1350 1355 1360

cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag 4128
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
1365 1370 1375

ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att 4176
Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
1380 1385 1390

gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg 4224
Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
1395 1400 1405

cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg 4272

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Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
   1410                    1415                    1420

aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc     4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425                1430                1435                1440

cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg     4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
                1445                1450                1455

ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg     4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
            1460                1465                1470

ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc     4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
        1475                1480                1485

tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt     4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
    1490                1495                1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt     4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505                1510                1515                1520

cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc     4608
Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                1525                1530                1535

cta cga aga ctg gag aaa aag aga agg agt aag gag aag cag atg gct     4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln Met Ala
            1540                1545                1550

gaa gcc cag tgc aaa cct tac tac tcc gac tac tcc cgc ttc cgg ctc     4704
Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu
        1555                1560                1565

ctc gtc cac cac ttg tgc acc agc cac tac ctg gac ctc ttc atc aca     4752
Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr
    1570                1575                1580

ggt gtc atc ggg ctg aac gtg gtc acc atg gcc atg gag cac tac cag     4800
Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln
1585                1590                1595                1600

cag ccc cag att ctg gat gag gct ctg aag atc tgc aac tac atc ttc     4848
Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe
                1605                1610                1615

act gtc atc ttt gtc ttg gag tca gtt ttc aaa ctt gtg gcc ttt ggt     4896
Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly
            1620                1625                1630

ttc cgt cgg ttc ttc cag gac agg tgg aac cag ctg gac ctg gcc att     4944
Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile
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gtg ctg ctg tcc atc atg ggc atc acg ctg gag gaa atc gag gtc aac     4992
Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn
    1650                1655                1660

gcc tcg ctg ccc atc aac ccc acc atc atc cgc atc atg agg gtg ctg     5040
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Ala Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu
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cgc att gcc cga gtg ctg aag ctg ctg aag atg gct gtg ggc atg cgg    5088
Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg
                1685                1690                1695

gcg ctg ctg gac acg gtg atg cag gcc ctg ccc cag gtg ggg aac ctg    5136
Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu
            1700                1705                1710

gga ctt ctc ttc atg ttg ttg ttt ttc atc ttt gca gct ctg ggc gtg    5184
Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val
        1715                1720                1725

gag ctc ttt gga gac ctg gag tgt gac gag aca cac ccc tgt gag ggc    5232
Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly
    1730                1735                1740

ctg ggc cgt cat gcc acc ttt cgg aac ttt ggc atg gcc ttc cta acc    5280
Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr
1745                1750                1755                1760

ctc ttc cga gtc tcc aca ggt gac aat tgg aat ggc att atg aag gac    5328
Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp
                1765                1770                1775

acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac acg gtc atc    5376
Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile
            1780                1785                1790

tcg cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttc gtg cta    5424
Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu
        1795                1800                1805

gtc aac gtg gtg atc gcc gtg ctg atg aag cac ctg gag gag agc aac    5472
Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn
    1810                1815                1820

aag gag gcc aag gag gag gcc gag cta gag gct gag ctg gag ctg gag    5520
Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu
1825                1830                1835                1840

atg aag acc ctc agc ccc cag ccc cac tcg cca ctg ggc agc ccc ttc    5568
Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe
                1845                1850                1855

ctc tgg cct ggg gtc gag ggc ccc gac agc ccc gac agc ccc aag cct    5616
Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro
            1860                1865                1870

ggg gct ctg cac cca gcg gcc cac gcg aga tca gcc tcc cac ttt tcc    5664
Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His Phe Ser
        1875                1880                1885

ctg gag cac ccc acg atg cag ccc cac ccc acg gag ctg cca gga cca    5712
Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro
    1890                1895                1900

gac tta ctg act gtg cgg aag tct ggg gtc agc cga acg cac tct ctg    5760
Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
1905                1910                1915                1920

ccc aat gac agc tac atg tgt cgg cat ggg agc act gcc gag ggg ccc    5808
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Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu Gly Pro
                1925                1930                1935

ctg gga cac agg ggc tgg ggg ctc ccc aaa gct cag tca ggc tcc gtc    5856
Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val
            1940                1945                1950

ttg tcc gtt cac tcc cag cca gca gat acc agc tac atc ctg cag ctt    5904
Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu
        1955                1960                1965

ccc aaa gat gca cct cat ctg ctc cag ccc cac agc gcc cca acc tgg    5952
Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro Thr Trp
    1970                1975                1980

ggc acc atc ccc aaa ctg ccc cca cca gga cgc tcc cct ttg gct cag    6000
Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln
1985                1990                1995                2000

agg cca ctc agg cgc cag gca gca ata agg act gac tcc ttg gac gtt    6048
Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
                2005                2010                2015

cag ggt ctg ggc agc cgg gaa gac ctg ctg gca gag gtg agt ggg ccc    6096
Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro
            2020                2025                2030

tcc ccg ccc ctg gcc cgg gcc tac tct ttc tgg ggc cag tca agt acc    6144
Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr
        2035                2040                2045

cag gca cag cag cac tcc cgc agc cac agc aag atc tcc aag cac atg    6192
Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys His Met
    2050                2055                2060

acc ccg cca gcc cct tgc cca ggc cca gaa ccc aac tgg ggc aag ggc    6240
Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly
2065                2070                2075                2080

cct cca gag acc aga agc agc tta gag ttg gac acg gag ctg agc tgg    6288
Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
                2085                2090                2095

att tca gga gac ctc ctg ccc cct ggc ggc cag gag gag ccc cca tcc    6336
Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Glu Pro Pro Ser
            2100                2105                2110

cca cgg gac ctg aag aag tgc tac agc gtg gag gcc cag agc tgc cag    6384
Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln
        2115                2120                2125

cgc cgg cct acg tcc tgg ctg gat gag cag agg aga cac tct atc gcc    6432
Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala
    2130                2135                2140

gtc agc tgc ctg gac agc ggc tcc caa ccc cac ctg ggc aca gac ccc    6480
Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro
2145                2150                2155                2160

tct aac ctt ggg ggc cag cct ctt ggg ggg cct ggg agc cgg ccc aag    6528
Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys
                2165                2170                2175

aaa aaa ctc agc ccg cct agt atc acc ata gac ccc ccc gag agc caa    6576
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Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Pro Glu Ser Gln
        2180                2185                2190

ggt cct cgg acc ccg ccc agc cct ggt atc tgc ctc cgg agg agg gct    6624
Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg Arg Ala
    2195                2200                2205

ccg tcc agc gac tcc aag gat ccc ttg gcc tct ggc ccc cct gac agc    6672
Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro Asp Ser
2210                2215                2220

atg gct gcc tcg ccc tcc cca aag aaa gat gtg ctg agt ctc tcc ggt    6720
Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu Ser Gly
2225                2230                2235                2240

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Leu Ser Ser Asp Pro Ala Asp Leu Asp Pro
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Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
             20                  25                  30

ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg     144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
         35                  40                  45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg     192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
     50                  55                  60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac     240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
 65                  70                  75                  80

ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg     288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
                 85                  90                  95

acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag     336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt     384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa     432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
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    130                     135                     140

aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc    480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc    528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac    576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg    624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
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ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc    672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
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Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

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Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc    816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
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cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg    864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
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Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
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tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac    960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac    1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
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ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg    1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
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ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc    1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
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Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380

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Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
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Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
405 410 415

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Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
420 425 430

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Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
435 440 445

cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg 1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
450 455 460

ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc 1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465 470 475 480

agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac 1488
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
485 490 495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc 1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
500 505 510

agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg 1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
515 520 525

tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg 1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
530 535 540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac 1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545 550 555 560

tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca 1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
565 570 575

tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc 1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590

gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta 1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605

gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc 1872
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620

cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt 1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640

aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa 1968
Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys

645 650 655

gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg 2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
660 665 670

gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca 2064
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
675 680 685

gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac 2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
690 695 700

ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca 2160
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705 710 715 720

gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc 2208
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
725 730 735

cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc 2256
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
740 745 750

atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc 2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
755 760 765

gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc 2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
770 775 780

ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt 2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785 790 795 800

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc 2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
805 810 815

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg 2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
820 825 830

ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg 2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
835 840 845

ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac 2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
850 855 860

gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc 2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
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atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat 2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
885 890 895

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Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala

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atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc     2784
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
        915                     920                     925

ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc     2832
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
    930                     935                     940

att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc     2880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945                     950                     955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc     2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                     970                     975

gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac     2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                     985                     990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg     3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
        995                    1000                    1005

cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc     3072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                   1015                    1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc     3120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                   1030                    1035                1040

cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg     3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
               1045                    1050                    1055

gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc     3216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
           1060                    1065                    1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac     3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
       1075                    1080                    1085

agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag     3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
    1090                   1095                    1100

cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag     3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105                   1110                    1115                1120

gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc     3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
               1125                    1130                    1135

cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca     3456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
           1140                    1145                    1150

gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg     3504
Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
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        1155                1160                1165

tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc    3552
Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
   1170                1175                1180

ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac    3600
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185                1190                1195                1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg    3648
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
                1205                1210                1215

atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca    3696
Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
            1220                1225                1230

gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg    3744
Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
        1235                1240                1245

atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc    3792
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
   1250                1255                1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac    3840
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
1265                1270                1275                1280

agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca    3888
Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
                1285                1290                1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc    3936
Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
            1300                1305                1310

ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg    3984
Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
        1315                1320                1325

ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct    4032
Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
   1330                1335                1340

gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg    4080
Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
1345                1350                1355                1360

cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag    4128
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
                1365                1370                1375

ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att    4176
Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
            1380                1385                1390

gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg    4224
Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
        1395                1400                1405

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Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
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aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc    4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425                1430                1435                1440

cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg    4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
                1445                1450                1455

ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg    4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
            1460                1465                1470

ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc    4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
        1475                1480                1485

tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt    4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
    1490                1495                1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt    4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505                1510                1515                1520

cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc    4608
Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                1525                1530                1535

cta cga aga ctg gag aaa aag aga agg aat cta atg ctg gac gat gta    4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp Asp Val
            1540                1545                1550

att gct tcc ggc agc tca gcc agc gct gcg tca gaa gcc cag tgc aaa    4704
Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln Cys Lys
        1555                1560                1565

cct tac tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac cac ttg    4752
Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu
    1570                1575                1580

tgc acc agc cac tac ctg gac ctc ttc atc aca ggt gtc atc ggg ctg    4800
Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu
1585                1590                1595                1600

aac gtg gtc acc atg gcc atg gag cac tac cag cag ccc cag att ctg    4848
Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu
                1605                1610                1615

gat gag gct ctg aag atc tgc aac tac atc ttc act gtc atc ttt gtc    4896
Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val
            1620                1625                1630

ttg gag tca gtt ttc aaa ctt gtg gcc ttt ggt ttc cgt cgg ttc ttc    4944
Leu Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe
        1635                1640                1645

cag gac agg tgg aac cag ctg gac ctg gcc att gtg ctg ctg tcc atc    4992
Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile
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atg ggc atc acg ctg gag gaa atc gag gtc aac gcc tcg ctg ccc atc    5040
Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Ala Ser Leu Pro Ile
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aac ccc acc atc atc cgc atc atg agg gtg ctg cgc att gcc cga gtg    5088
Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val
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ctg aag ctg ctg aag atg gct gtg ggc atg cgg gcg ctg ctg gac acg    5136
Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu Asp Thr
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gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg    5184
Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met
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ttg ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac    5232
Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp
    1730                1735                1740

ctg gag tgt gac gag aca cac ccc tgt gag ggc ctg ggc cgt cat gcc    5280
Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala
1745                1750                1755                1760

acc ttt cgg aac ttt ggc atg gcc ttc cta acc ctc ttc cga gtc tcc    5328
Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser
                1765                1770                1775

aca ggt gac aat tgg aat ggc att atg aag gac acc ctc cgg gac tgt    5376
Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys
            1780                1785                1790

gac cag gag tcc acc tgc tac aac acg gtc atc tcg cct atc tac ttt    5424
Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe
        1795                1800                1805

gtg tcc ttc gtg ctg acg gcc cag ttc gtg cta gtc aac gtg gtg atc    5472
Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile
    1810                1815                1820

gcc gtg ctg atg aag cac ctg gag gag agc aac aag gag gcc aag gag    5520
Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu
1825                1830                1835                1840

gag gcc gag cta gag gct gag ctg gag ctg gag atg aag acc ctc agc    5568
Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser
                1845                1850                1855

ccc cag ccc cac tcg cca ctg ggc agc ccc ttc ctc tgg cct ggg gtc    5616
Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val
            1860                1865                1870

gag ggc ccc gac agc ccc gac agc ccc aag cct ggg gct ctg cac cca    5664
Glu Gly Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro
        1875                1880                1885

gcg gcc cac gcg aga tca gcc tcc cac ttt tcc ctg gag cac ccc acg    5712
Ala Ala His Ala Arg Ser Ala Ser His Phe Ser Leu Glu His Pro Thr
    1890                1895                1900

atg cag ccc cac ccc acg gag ctg cca gga cca gac tta ctg act gtg    5760
Met Gln Pro His Pro Thr Glu Leu Pro Gly Pro Asp Leu Leu Thr Val
1905                1910                1915                1920

cgg aag tct ggg gtc agc cga acg cac tct ctg ccc aat gac agc tac    5808
Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr
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atg tgt cgg cat ggg agc act gcc gag ggg ccc ctg gga cac agg ggc    5856
Met Cys Arg His Gly Ser Thr Ala Glu Gly Pro Leu Gly His Arg Gly
            1940                1945                1950

tgg ggg ctc ccc aaa gct cag tca ggc tcc gtc ttg tcc gtt cac tcc    5904
Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser
        1955                1960                1965

cag cca gca gat acc agc tac atc ctg cag ctt ccc aaa gat gca cct    5952
Gln Pro Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro
    1970                1975                1980

cat ctg ctc cag ccc cac agc gcc cca acc tgg ggc acc atc ccc aaa    6000
His Leu Leu Gln Pro His Ser Ala Pro Thr Trp Gly Thr Ile Pro Lys
1985                1990                1995                2000

ctg ccc cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc    6048
Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg
            2005                2010                2015

cag gca gca ata agg act gac tcc ttg gac gtt cag ggt ctg ggc agc    6096
Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser
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cgg gaa gac ctg ctg gca gag gtg agt ggg ccc tcc ccg ccc ctg gcc    6144
Arg Glu Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala
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cgg gcc tac tct ttc tgg ggc cag tca agt acc cag gca cag cag cac    6192
Arg Ala Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His
    2050                2055                2060

tcc cgc agc cac agc aag atc tcc aag cac atg acc ccg cca gcc cct    6240
Ser Arg Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro
2065                2070                2075                2080

tgc cca ggc cca gaa ccc aac tgg ggc aag ggc cct cca gag acc aga    6288
Cys Pro Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg
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agc agc tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctc    6336
Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu
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ctg ccc cct ggc ggc cag gag gag ccc cca tcc cca cgg gac ctg aag    6384
Leu Pro Pro Gly Gly Gln Glu Glu Pro Pro Ser Pro Arg Asp Leu Lys
        2115                2120                2125

aag tgc tac agc gtg gag gcc cag agc tgc cag cgc cgg cct acg tcc    6432
Lys Cys Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Arg Pro Thr Ser
    2130                2135                2140

tgg ctg gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac    6480
Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp
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agc ggc tcc caa ccc cac ctg ggc aca gac ccc tct aac ctt ggg ggc    6528
Ser Gly Ser Gln Pro His Leu Gly Thr Asp Pro Ser Asn Leu Gly Gly
            2165                2170                2175

cag cct ctt ggg ggg cct ggg agc cgg ccc aag aaa aaa ctc agc ccg    6576
Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro
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35 40 45

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Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
50 55 60

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Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65 70 75 80

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Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
85 90 95

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Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
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115 120 125

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gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa      432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc      480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc      528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac      576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg      624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc      672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga      720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag      768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc      816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg      864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc      912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290                 295                 300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac      960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac     1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg     1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc     1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365

ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc     1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380
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ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag 1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385 390 395 400

acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc 1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
405 410 415

ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc 1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
420 425 430

tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc 1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
435 440 445

cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg 1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
450 455 460

ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc 1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465 470 475 480

agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac 1488
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
485 490 495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc 1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
500 505 510

agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg 1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
515 520 525

tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg 1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
530 535 540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac 1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545 550 555 560

tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca 1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
565 570 575

tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc 1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
580 585 590

gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta 1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
595 600 605

gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc 1872
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
610 615 620

cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt 1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640

aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa 1968
Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
645 650 655

gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg 2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
660 665 670

gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca 2064
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
675 680 685

gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac 2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
690 695 700

ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca 2160
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705 710 715 720

gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc 2208
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
725 730 735

cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc 2256
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
740 745 750

atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc 2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
755 760 765

gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc 2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
770 775 780

ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt 2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785 790 795 800

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc 2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
805 810 815

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg 2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
820 825 830

ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg 2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
835 840 845

ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac 2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
850 855 860

gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc 2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865 870 875 880

atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat 2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
885 890 895

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ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc   2736
Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
            900                 905                 910

atc gtc act gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc   2784
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
        915                 920                 925

ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc   2832
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
    930                 935                 940

att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc   2880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945                 950                 955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc   2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                 970                 975

gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac   2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                 985                 990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg   3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
        995                 1000                1005

cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc   3072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                1015                1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc   3120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                1030                1035                1040

cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg   3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                1045                1050                1055

gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc   3216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060                1065                1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac   3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
        1075                1080                1085

agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag   3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
    1090                1095                1100

cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag   3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105                1110                1115                1120

gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc   3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                1125                1130                1135

cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca   3456
His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro
            1140                1145                1150
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gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg 3504
Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly
1155 1160 1165

tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc 3552
Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg
1170 1175 1180

ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac 3600
Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp
1185 1190 1195 1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg 3648
Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp
1205 1210 1215

atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca 3696
Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser
1220 1225 1230

gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg 3744
Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg
1235 1240 1245

atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc 3792
Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe
1250 1255 1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac 3840
Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His
1265 1270 1275 1280

agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca 3888
Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala
1285 1290 1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc 3936
Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys
1300 1305 1310

ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg 3984
Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly
1315 1320 1325

ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct 4032
Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser
1330 1335 1340

gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg 4080
Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu
1345 1350 1355 1360

cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag 4128
Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys
1365 1370 1375

ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att 4176
Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile
1380 1385 1390

gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg 4224
Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
1395 1400 1405

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cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg   4272
Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
    1410                1415                1420

aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc   4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425                1430                1435                1440

cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg   4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
                1445                1450                1455

ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg   4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
            1460                1465                1470

ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc   4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
        1475                1480                1485

tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt   4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
    1490                1495                1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt   4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505                1510                1515                1520

cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc   4608
Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
                1525                1530                1535

cta cga aga ctg gag aaa aag aga agg agt aag gag aag cag atg gct   4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln Met Ala
            1540                1545                1550

gat cta atg ctg gac gat gta att gct tcc ggc agc tca gcc agc gct   4704
Asp Leu Met Leu Asp Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala
        1555                1560                1565

gcg tca gaa gcc cag tgc aaa cct tac tac tcc gac tac tcc cgc ttc   4752
Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe
    1570                1575                1580

cgg ctc ctc gtc cac cac ttg tgc acc agc cac tac ctg gac ctc ttc   4800
Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe
1585                1590                1595                1600

atc aca ggt gtc atc ggg ctg aac gtg gtc acc atg gcc atg gag cac   4848
Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His
                1605                1610                1615

tac cag cag ccc cag att ctg gat gag gct ctg aag atc tgc aac tac   4896
Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr
            1620                1625                1630

atc ttc act gtc atc ttt gtc ttg gag tca gtt ttc aaa ctt gtg gcc   4944
Ile Phe Thr Val Ile Phe Val Leu Glu Ser Val Phe Lys Leu Val Ala
        1635                1640                1645

ttt ggt ttc cgt cgg ttc ttc cag gac agg tgg aac cag ctg gac ctg   4992
Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu
    1650                1655                1660
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gcc att gtg ctg ctg tcc atc atg ggc atc acg ctg gag gaa atc gag    5040
Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu
1665                1670                1675                1680

gtc aac gcc tcg ctg ccc atc aac ccc acc atc atc cgc atc atg agg    5088
Val Asn Ala Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg
                1685                1690                1695

gtg ctg cgc att gcc cga gtg ctg aag ctg ctg aag atg gct gtg ggc    5136
Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly
            1700                1705                1710

atg cgg gcg ctg ctg gac acg gtg atg cag gcc ctg ccc cag gtg ggg    5184
Met Arg Ala Leu Leu Asp Thr Val Met Gln Ala Leu Pro Gln Val Gly
        1715                1720                1725

aac ctg gga ctt ctc ttc atg ttg ttg ttt ttc atc ttt gca gct ctg    5232
Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu
    1730                1735                1740

ggc gtg gag ctc ttt gga gac ctg gag tgt gac gag aca cac ccc tgt    5280
Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys
1745                1750                1755                1760

gag ggc ctg ggc cgt cat gcc acc ttt cgg aac ttt ggc atg gcc ttc    5328
Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe
                1765                1770                1775

cta acc ctc ttc cga gtc tcc aca ggt gac aat tgg aat ggc att atg    5376
Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met
            1780                1785                1790

aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac acg    5424
Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr
        1795                1800                1805

gtc atc tcg cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttc    5472
Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe
    1810                1815                1820

gtg cta gtc aac gtg gtg atc gcc gtg ctg atg aag cac ctg gag gag    5520
Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu
1825                1830                1835                1840

agc aac aag gag gcc aag gag gag gcc gag cta gag gct gag ctg gag    5568
Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu
                1845                1850                1855

ctg gag atg aag acc ctc agc ccc cag ccc cac tcg cca ctg ggc agc    5616
Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser
            1860                1865                1870

ccc ttc ctc tgg cct ggg gtc gag ggc ccc gac agc ccc gac agc ccc    5664
Pro Phe Leu Trp Pro Gly Val Glu Gly Pro Asp Ser Pro Asp Ser Pro
        1875                1880                1885

aag cct ggg gct ctg cac cca gcg gcc cac gcg aga tca gcc tcc cac    5712
Lys Pro Gly Ala Leu His Pro Ala Ala His Ala Arg Ser Ala Ser His
    1890                1895                1900

ttt tcc ctg gag cac ccc acg atg cag ccc cac ccc acg gag ctg cca    5760
Phe Ser Leu Glu His Pro Thr Met Gln Pro His Pro Thr Glu Leu Pro
1905                1910                1915                1920
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gga cca gac tta ctg act gtg cgg aag tct ggg gtc agc cga acg cac 5808
Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His
1925 1930 1935

tct ctg ccc aat gac agc tac atg tgt cgg cat ggg agc act gcc gag 5856
Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg His Gly Ser Thr Ala Glu
1940 1945 1950

ggg ccc ctg gga cac agg ggc tgg ggg ctc ccc aaa gct cag tca ggc 5904
Gly Pro Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly
1955 1960 1965

tcc gtc ttg tcc gtt cac tcc cag cca gca gat acc agc tac atc ctg 5952
Ser Val Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Tyr Ile Leu
1970 1975 1980

cag ctt ccc aaa gat gca cct cat ctg ctc cag ccc cac agc gcc cca 6000
Gln Leu Pro Lys Asp Ala Pro His Leu Leu Gln Pro His Ser Ala Pro
1985 1990 1995 2000

acc tgg ggc acc atc ccc aaa ctg ccc cca cca gga cgc tcc cct ttg 6048
Thr Trp Gly Thr Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu
2005 2010 2015

gct cag agg cca ctc agg cgc cag gca gca ata agg act gac tcc ttg 6096
Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu
2020 2025 2030

gac gtt cag ggt ctg ggc agc cgg gaa gac ctg ctg gca gag gtg agt 6144
Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ala Glu Val Ser
2035 2040 2045

ggg ccc tcc ccg ccc ctg gcc cgg gcc tac tct ttc tgg ggc cag tca 6192
Gly Pro Ser Pro Pro Leu Ala Arg Ala Tyr Ser Phe Trp Gly Gln Ser
2050 2055 2060

agt acc cag gca cag cag cac tcc cgc agc cac agc aag atc tcc aag 6240
Ser Thr Gln Ala Gln Gln His Ser Arg Ser His Ser Lys Ile Ser Lys
2065 2070 2075 2080

cac atg acc ccg cca gcc cct tgc cca ggc cca gaa ccc aac tgg ggc 6288
His Met Thr Pro Pro Ala Pro Cys Pro Gly Pro Glu Pro Asn Trp Gly
2085 2090 2095

aag ggc cct cca gag acc aga agc agc tta gag ttg gac acg gag ctg 6336
Lys Gly Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu
2100 2105 2110

agc tgg att tca gga gac ctc ctg ccc cct ggc ggc cag gag gag ccc 6384
Ser Trp Ile Ser Gly Asp Leu Leu Pro Pro Gly Gly Gln Glu Glu Pro
2115 2120 2125

cca tcc cca cgg gac ctg aag aag tgc tac agc gtg gag gcc cag agc 6432
Pro Ser Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Ala Gln Ser
2130 2135 2140

tgc cag cgc cgg cct acg tcc tgg ctg gat gag cag agg aga cac tct 6480
Cys Gln Arg Arg Pro Thr Ser Trp Leu Asp Glu Gln Arg Arg His Ser
2145 2150 2155 2160

atc gcc gtc agc tgc ctg gac agc ggc tcc caa ccc cac ctg ggc aca 6528
Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro His Leu Gly Thr
2165 2170 2175

gac ccc tct aac ctt ggg ggc cag cct ctt ggg ggg cct ggg agc cgg 6576
Asp Pro Ser Asn Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg
2180 2185 2190

ccc aag aaa aaa ctc agc ccg cct agt atc acc ata gac ccc ccc gag 6624
Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Thr Ile Asp Pro Pro Glu
2195 2200 2205

agc caa ggt cct cgg acc ccg ccc agc cct ggt atc tgc ctc cgg agg 6672
Ser Gln Gly Pro Arg Thr Pro Pro Ser Pro Gly Ile Cys Leu Arg Arg
2210 2215 2220

agg gct ccg tcc agc gac tcc aag gat ccc ttg gcc tct ggc ccc cct 6720
Arg Ala Pro Ser Ser Asp Ser Lys Asp Pro Leu Ala Ser Gly Pro Pro
2225 2230 2235 2240

gac agc atg gct gcc tcg ccc tcc cca aag aaa gat gtg ctg agt ctc 6768
Asp Ser Met Ala Ala Ser Pro Ser Pro Lys Lys Asp Val Leu Ser Leu
2245 2250 2255

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Arg Ser Phe Met Arg Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Pro
20 25 30

ggg ccg ggg tca gca gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144
Gly Pro Gly Ser Ala Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
35 40 45

gag ggg ctg ccg tac ccg gcg ctg gcc ccg gtg gtt ttc ttc tac ttg 192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
50 55 60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac 240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65 70 75 80

ccc tgg ttt gag cgc atc agc atg ttg gtc atc ctt ctc aac tgc gtg 288
Pro Trp Phe Glu Arg Ile Ser Met Leu Val Ile Leu Leu Asn Cys Val
85 90 95

acc ctg ggc atg ttc cgg cca tgc gag gac atc gcc tgt gac tcc cag 336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
100 105 110

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cgc tgc cgg atc ctg cag gcc ttt gat gac ttc atc ttt gcc ttc ttt    384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

gcc gtg gag atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aaa    432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aag tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc atc gtc    480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

atc gca ggg atg ctg gag tac tcg ctg gac ctg cag aac gtc agc ttc    528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tca gct gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac    576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc atc ctt gtc acg ttg ctg ctg gat acg ctg    624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

ccc atg ctg ggc aac gtc ctg ctg ctc tgc ttc ttc gtc ttc ttc atc    672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttc ggc atc gtc ggc gtc cag ctg tgg gca ggg ctg ctt cgg aac cga    720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc cta cct gag aat ttc agc ctc ccc ctg agc gtg gac ctg gag    768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cgc tat tac cag aca gag aac gag gat gag agc ccc ttc atc tgc tcc    816
Arg Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cca cgc gag aac ggc atg cgg tcc tgc aga agc gtg ccc acg ctg    864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgc ggg gac ggg ggc ggt ggc cca cct tgc ggt ctg gac tat gag gcc    912
Arg Gly Asp Gly Gly Gly Gly Pro Pro Cys Gly Leu Asp Tyr Glu Ala
    290                 295                 300

tac aac agc tcc agc aac acc acc tgt gtc aac tgg aac cag tac tac    960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tca gcg ggg gag cac aac ccc ttc aag ggc gcc atc aac    1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc acg    1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttt gtg atg gat gct cat tcc    1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365
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ttc tac aat ttc atc tac ttc atc ctc ctc atc atc gtg ggc tcc ttc    1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                     380

ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tca gag    1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                     395                 400

acc aag cag cgg gaa agc cag ctg atg cgg gag cag cgt gtg cgg ttc    1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                     410                 415

ctg tcc aac gcc agc acc ctg gct agc ttc tct gag ccc ggc agc tgc    1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                     425                 430

tat gag gag ctg ctc aag tac ctg gtg tac atc ctt cgt aag gca gcc    1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                     440                 445

cgc agg ctg gct cag gtc tct cgg gca gca ggt gtg cgg gtt ggg ctg    1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ala Gly Val Arg Val Gly Leu
    450                     455                 460

ctc agc agc cca gca ccc ctc ggg ggc cag gag acc cag ccc agc agc    1440
Leu Ser Ser Pro Ala Pro Leu Gly Gly Gln Glu Thr Gln Pro Ser Ser
465                     470                 475                 480

agc tgc tct cgc tcc cac cgc cgc cta tcc gtc cac cac ctg gtg cac    1488
Ser Cys Ser Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                     490                 495

cac cac cac cac cat cac cac cac tac cac ctg ggc aat ggg acg ctc    1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                     505                 510

agg gcc ccc cgg gcc agc ccg gag atc cag gac agg gat gcc aat ggg    1584
Arg Ala Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                     520                 525

tcc cgc cgg ctc atg ctg cca cca ccc tcg acg cct gcc ctc tcc ggg    1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Ala Leu Ser Gly
    530                     535                 540

gcc ccc cct ggt ggc gca gag tct gtg cac agc ttc tac cat gcc gac    1680
Ala Pro Pro Gly Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                     550                 555                 560

tgc cac tta gag cca gtc cgc tgc cag gcg ccc cct ccc agg tcc cca    1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Ser Pro
                565                     570                 575

tct gag gca tcc ggc agg act gtg ggc agc ggg aag gtg tat ccc acc    1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                     585                 590

gtg cac acc agc cct cca ccg gag acg ctg aag gag aag gca cta gta    1824
Val His Thr Ser Pro Pro Pro Glu Thr Leu Lys Glu Lys Ala Leu Val
        595                     600                 605

gag gtg gct gcc agc tct ggg ccc cca acc ctc acc agc ctc aac atc    1872
Glu Val Ala Ala Ser Ser Gly Pro Pro Thr Leu Thr Ser Leu Asn Ile
    610                     615                 620
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cca ccc ggg ccc tac agc tcc atg cac aag ctg ctg gag aca cag agt   1920
Pro Pro Gly Pro Tyr Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640

aca ggt gcc tgc caa agc tct tgc aag atc tcc agc cct tgc ttg aaa   1968
Thr Gly Ala Cys Gln Ser Ser Cys Lys Ile Ser Ser Pro Cys Leu Lys
                645                 650                 655

gca gac agt gga gcc tgt ggt cca gac agc tgc ccc tac tgt gcc cgg   2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

gcc ggg gca ggg gag gtg gag ctc gcc gac cgt gaa atg cct gac tca   2064
Ala Gly Ala Gly Glu Val Glu Leu Ala Asp Arg Glu Met Pro Asp Ser
        675                 680                 685

gac agc gag gca gtt tat gag ttc aca cag gat gcc cag cac agc gac   2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gac ccc cac agc cgg cgg caa cgg agc ctg ggc cca gat gca   2160
Leu Arg Asp Pro His Ser Arg Arg Gln Arg Ser Leu Gly Pro Asp Ala
705                 710                 715                 720

gag ccc agc tct gtg ctg gcc ttc tgg agg cta atc tgt gac acc ttc   2208
Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr Phe
                725                 730                 735

cga aag att gtg gac agc aag tac ttt ggc cgg gga atc atg atc gcc   2256
Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile Ala
            740                 745                 750

atc ctg gtc aac aca ctc agc atg ggc atc gaa tac cac gag cag ccc   2304
Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln Pro
        755                 760                 765

gag gag ctt acc aac gcc cta gaa atc agc aac atc gtc ttc acc agc   2352
Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr Ser
    770                 775                 780

ctc ttt gcc ctg gag atg ctg ctg aag ctg ctt gtg tat ggt ccc ttt   2400
Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro Phe
785                 790                 795                 800

ggc tac atc aag aat ccc tac aac atc ttc gat ggt gtc att gtg gtc   2448
Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val Val
                805                 810                 815

atc agc gtg tgg gag atc gtg ggc cag cag ggg ggc ggc ctg tcg gtg   2496
Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser Val
            820                 825                 830

ctg cgg acc ttc cgc ctg atg cgt gtg ctg aag ctg gtg cgc ttc ctg   2544
Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe Leu
        835                 840                 845

ccg gcg ctg cag cgg cag ctg gtg gtg ctc atg aag acc atg gac aac   2592
Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp Asn
    850                 855                 860

gtg gcc acc ttc tgc atg ctg ctt atg ctc ttc atc ttc atc ttc agc   2640
Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser
865                 870                 875                 880
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atc ctg ggc atg cat ctc ttc ggc tgc aag ttt gcc tct gag cgg gat    2688
Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg Asp
                885                 890                 895

ggg gac acc ctg cca gac cgg aag aat ttt gac tcc ttg ctc tgg gcc    2736
Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
            900                 905                 910

atc gtc acc gtc ttt cag atc ctg acc cag gag gac tgg aac aaa gtc    2784
Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys Val
        915                 920                 925

ctc tac aat ggt atg gcc tcc acg tcg tcc tgg gcg gcc ctt tat ttc    2832
Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr Phe
    930                 935                 940

att gcc ctc atg acc ttc ggc aac tac gtg ctc ttc aat ttg ctg gtc    2880
Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu Val
945                 950                 955                 960

gcc att ctg gtg gag ggc ttc cag gcg gag gga gat gcc aac aag tcc    2928
Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn Lys Ser
                965                 970                 975

gaa tca gag ccc gat ttc ttc tca ccc agc ctg gat ggt gat ggg gac    2976
Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Leu Asp Gly Asp Gly Asp
            980                 985                 990

agg aag aag tgc ttg gcc ttg gtg tcc ctg gga gag cac ccg gag ctg    3024
Arg Lys Lys Cys Leu Ala Leu Val Ser Leu Gly Glu His Pro Glu Leu
        995                 1000                1005

cgg aag agc ctg ctg ccg cct ctc atc atc cac acg gcc gcc aca ccc    3072
Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr Pro
    1010                1015                1020

atg tcg ctg ccc aag agc acc agc acg ggc ctg ggc gag gcg ctg ggc    3120
Met Ser Leu Pro Lys Ser Thr Ser Thr Gly Leu Gly Glu Ala Leu Gly
1025                1030                1035                1040

cct gcg tcg cgc cgc acc agc agc agc ggg tcg gca gag cct ggg gcg    3168
Pro Ala Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly Ala
                1045                1050                1055

gcc cac gag atg aag tca ccg ccc agc gcc cgc agc tct ccg cac agc    3216
Ala His Glu Met Lys Ser Pro Pro Ser Ala Arg Ser Ser Pro His Ser
            1060                1065                1070

ccc tgg agc gct gca agc agc tgg acc agc agg cgc tcc agc cgg aac    3264
Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser Arg Asn
        1075                1080                1085

agc ctc ggc cgt gca ccc agc ctg aag cgg aga agc cca agt gga gag    3312
Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser Gly Glu
    1090                1095                1100

cgg cgg tcc ctg ttg tcg gga gaa ggc cag gag agc cag gat gaa gag    3360
Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp Glu Glu
1105                1110                1115                1120

gag agc tca gaa gag gag cgg gcc agc cct gcg ggc agt gac cat cgc    3408
Glu Ser Ser Glu Glu Glu Arg Ala Ser Pro Ala Gly Ser Asp His Arg
                1125                1130                1135
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cac agg ggg tcc ctg gag cgg gag gcc aag agt tcc ttt gac ctg cca 3456

His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp Leu Pro

1140 1145 1150

gac aca ctg cag gtg cca ggg ctg cat cgc act gcc agt ggc cga ggg 3504

Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly Arg Gly

1155 1160 1165

tct gct tct gag cac cag gac tgc aat ggc aag tcg gct tca ggg cgc 3552

Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser Gly Arg

1170 1175 1180

ctg gcc cgg gcc ctg cgg cct gat gac ccc cca ctg gat ggg gat gac 3600

Leu Ala Arg Ala Leu Arg Pro Asp Asp Pro Pro Leu Asp Gly Asp Asp

1185 1190 1195 1200

gcc gat gac gag ggc aac ctg agc aaa ggg gaa cgg gtc cgc gcg tgg 3648

Ala Asp Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Val Arg Ala Trp

1205 1210 1215

atc cga gcc cga ctc cct gcc tgc tgc ctc gag cga gac tcc tgg tca 3696

Ile Arg Ala Arg Leu Pro Ala Cys Cys Leu Glu Arg Asp Ser Trp Ser

1220 1225 1230

gcc tac atc ttc cct cct cag tcc agg ttc cgc ctc ctg tgt cac cgg 3744

Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys His Arg

1235 1240 1245

atc atc acc cac aag atg ttc gac cac gtg gtc ctt gtc atc atc ttc 3792

Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile Ile Phe

1250 1255 1260

ctt aac tgc atc acc atc gcc atg gag cgc ccc aaa att gac ccc cac 3840

Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp Pro His

1265 1270 1275 1280

agc gct gaa cgc atc ttc ctg acc ctc tcc aat tac atc ttc acc gca 3888

Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe Thr Ala

1285 1290 1295

gtc ttt ctg gct gaa atg aca gtg aag gtg gtg gca ctg ggc tgg tgc 3936

Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly Trp Cys

1300 1305 1310

ttc ggg gag cag gcg tac ctg cgg agc agt tgg aac gtg ctg gac ggg 3984

Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu Asp Gly

1315 1320 1325

ctg ttg gtg ctc atc tcc gtc atc gac att ctg gtg tcc atg gtc tct 4032

Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met Val Ser

1330 1335 1340

gac agc ggc acc aag atc ctg ggc atg ctg agg gtg ctg cgg ctg ctg 4080

Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg Leu Leu

1345 1350 1355 1360

cgg acc ctg cgc ccg ctc agg gtg atc agc cgg gcg cag ggg ctg aag 4128

Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly Leu Lys

1365 1370 1375

ctg gtg gtg gag acg ctg atg tcc tca ctg aaa ccc atc ggc aac att 4176

Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly Asn Ile

1380 1385 1390

gta gtc atc tgc tgt gcc ttc ttc atc att ttc ggc atc ttg ggg gtg 4224
Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu Gly Val
1395 1400 1405

cag ctc ttc aaa ggg aag ttt ttc gtg tgc cag ggc gag gat acc agg 4272
Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp Thr Arg
1410 1415 1420

aac atc acc aat aaa tcg gac tgt gcc gag gcc agt tac cgg tgg gtc 4320
Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg Trp Val
1425 1430 1435 1440

cgg cac aag tac aac ttt gac aac ctt ggc cag gcc ctg atg tcc ctg 4368
Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met Ser Leu
1445 1450 1455

ttc gtt ttg gcc tcc aag gat ggt tgg gtg gac atc atg tac gat ggg 4416
Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr Asp Gly
1460 1465 1470

ctg gat gct gtg ggc gtg gac cag cag ccc atc atg aac cac aac ccc 4464
Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His Asn Pro
1475 1480 1485

tgg atg ctg ctg tac ttc atc tcg ttc ctg ctc att gtg gcc ttc ttt 4512
Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala Phe Phe
1490 1495 1500

gtc ctg aac atg ttt gtg ggt gtg gtg gtg gag aac ttc cac aag tgt 4560
Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His Lys Cys
1505 1510 1515 1520

cgg cag cac cag gag gaa gag gag gcc cgg cgg cgg gag gag aag cgc 4608
Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg
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cta cga aga ctg gag aaa aag aga agg aaa gcc cag tgc aaa cct tac 4656
Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Cys Lys Pro Tyr
1540 1545 1550

tac tcc gac tac tcc cgc ttc cgg ctc ctc gtc cac cac ttg tgc acc 4704
Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu Cys Thr
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agc cac tac ctg gac ctc ttc atc aca ggt gtc atc ggg ctg aac gtg 4752
Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val
1570 1575 1580

gtc acc atg gcc atg gag cac tac cag cag ccc cag att ctg gat gag 4800
Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu
1585 1590 1595 1600

gct ctg aag atc tgc aac tac atc ttc act gtc atc ttt gtc ttg gag 4848
Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val Leu Glu
1605 1610 1615

tca gtt ttc aaa ctt gtg gcc ttt ggt ttc cgt cgg ttc ttc cag gac 4896
Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Gln Asp
1620 1625 1630

agg tgg aac cag ctg gac ctg gcc att gtg ctg ctg tcc atc atg ggc 4944
Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly
1635 1640 1645

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atc acg ctg gag gaa atc gag gtc aac gcc tcg ctg ccc atc aac ccc    4992
Ile Thr Leu Glu Glu Ile Glu Val Asn Ala Ser Leu Pro Ile Asn Pro
   1650                1655                1660

acc atc atc cgc atc atg agg gtg ctg cgc att gcc cga gtg ctg aag    5040
Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys
1665                1670                1675                1680

ctg ctg aag atg gct gtg ggc atg cgg gcg ctg ctg gac acg gtg atg    5088
Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu Asp Thr Val Met
               1685                1690                1695

cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc ttc atg ttg ttg    5136
Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu
           1700                1705                1710

ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac ctg gag    5184
Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu
       1715                1720                1725

tgt gac gag aca cac ccc tgt gag ggc ctg ggc cgt cat gcc acc ttt    5232
Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe
   1730                1735                1740

cgg aac ttt ggc atg gcc ttc cta acc ctc ttc cga gtc tcc aca ggt    5280
Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly
1745                1750                1755                1760

gac aat tgg aat ggc att atg aag gac acc ctc cgg gac tgt gac cag    5328
Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln
               1765                1770                1775

gag tcc acc tgc tac aac acg gtc atc tcg cct atc tac ttt gtg tcc    5376
Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser
           1780                1785                1790

ttc gtg ctg acg gcc cag ttc gtg cta gtc aac gtg gtg atc gcc gtg    5424
Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile Ala Val
       1795                1800                1805

ctg atg aag cac ctg gag gag agc aac aag gag gcc aag gag gag gcc    5472
Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala
   1810                1815                1820

gag cta gag gct gag ctg gag ctg gag atg aag acc ctc agc ccc cag    5520
Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln
1825                1830                1835                1840

ccc cac tcg cca ctg ggc agc ccc ttc ctc tgg cct ggg gtc gag ggc    5568
Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly
               1845                1850                1855

ccc gac agc ccc gac agc ccc aag cct ggg gct ctg cac cca gcg gcc    5616
Pro Asp Ser Pro Asp Ser Pro Lys Pro Gly Ala Leu His Pro Ala Ala
           1860                1865                1870

cac gcg aga tca gcc tcc cac ttt tcc ctg gag cac ccc acg atg cag    5664
His Ala Arg Ser Ala Ser His Phe Ser Leu Glu His Pro Thr Met Gln
       1875                1880                1885

ccc cac ccc acg gag ctg cca gga cca gac tta ctg act gtg cgg aag    5712
Pro His Pro Thr Glu Leu Pro Gly Pro Asp Leu Leu Thr Val Arg Lys
   1890                1895                1900
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tct ggg gtc agc cga acg cac tct ctg ccc aat gac agc tac atg tgt 5760
Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys
1905 1910 1915 1920

cgg cat ggg agc act gcc gag ggg ccc ctg gga cac agg ggc tgg ggg 5808
Arg His Gly Ser Thr Ala Glu Gly Pro Leu Gly His Arg Gly Trp Gly
1925 1930 1935

ctc ccc aaa gct cag tca ggc tcc gtc ttg tcc gtt cac tcc cag cca 5856
Leu Pro Lys Ala Gln Ser Gly Ser Val Leu Ser Val His Ser Gln Pro
1940 1945 1950

gca gat acc agc tac atc ctg cag ctt ccc aaa gat gca cct cat ctg 5904
Ala Asp Thr Ser Tyr Ile Leu Gln Leu Pro Lys Asp Ala Pro His Leu
1955 1960 1965

ctc cag ccc cac agc gcc cca acc tgg ggc acc atc ccc aaa ctg ccc 5952
Leu Gln Pro His Ser Ala Pro Thr Trp Gly Thr Ile Pro Lys Leu Pro
1970 1975 1980

cca cca gga cgc tcc cct ttg gct cag agg cca ctc agg cgc cag gca 6000
Pro Pro Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala
1985 1990 1995 2000

gca ata agg act gac tcc ttg gac gtt cag ggt ctg ggc agc cgg gaa 6048
Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu
2005 2010 2015

gac ctg ctg gca gag gtg agt ggg ccc tcc ccg ccc ctg gcc cgg gcc 6096
Asp Leu Leu Ala Glu Val Ser Gly Pro Ser Pro Pro Leu Ala Arg Ala
2020 2025 2030

tac tct ttc tgg ggc cag tca agt acc cag gca cag cag cac tcc cgc 6144
Tyr Ser Phe Trp Gly Gln Ser Ser Thr Gln Ala Gln Gln His Ser Arg
2035 2040 2045

agc cac agc aag atc tcc aag cac atg acc ccg cca gcc cct tgc cca 6192
Ser His Ser Lys Ile Ser Lys His Met Thr Pro Pro Ala Pro Cys Pro
2050 2055 2060

ggc cca gaa ccc aac tgg ggc aag ggc cct cca gag acc aga agc agc 6240
Gly Pro Glu Pro Asn Trp Gly Lys Gly Pro Pro Glu Thr Arg Ser Ser
2065 2070 2075 2080

tta gag ttg gac acg gag ctg agc tgg att tca gga gac ctc ctg ccc 6288
Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro
2085 2090 2095

cct ggc ggc cag gag gag ccc cca tcc cca cgg gac ctg aag aag tgc 6336
Pro Gly Gly Gln Glu Glu Pro Pro Ser Pro Arg Asp Leu Lys Lys Cys
2100 2105 2110

tac agc gtg gag gcc cag agc tgc cag cgc cgg cct acg tcc tgg ctg 6384
Tyr Ser Val Glu Ala Gln Ser Cys Gln Arg Arg Pro Thr Ser Trp Leu
2115 2120 2125

gat gag cag agg aga cac tct atc gcc gtc agc tgc ctg gac agc ggc 6432
Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly
2130 2135 2140

tcc caa ccc cac ctg ggc aca gac ccc tct aac ctt ggg ggc cag cct 6480
Ser Gln Pro His Leu Gly Thr Asp Pro Ser Asn Leu Gly Gly Gln Pro
2145 2150 2155 2160

ctt ggg ggg cct ggg agc cgg ccc aag aaa aaa ctc agc ccg cct agt 6528
Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser
2165 2170 2175

atc acc ata gac ccc ccc gag agc caa ggt cct cgg acc ccg ccc agc 6576
Ile Thr Ile Asp Pro Pro Glu Ser Gln Gly Pro Arg Thr Pro Pro Ser
2180 2185 2190

cct ggt atc tgc ctc cgg agg agg gct ccg tcc agc gac tcc aag gat 6624
Pro Gly Ile Cys Leu Arg Arg Arg Ala Pro Ser Ser Asp Ser Lys Asp
2195 2200 2205

ccc ttg gcc tct ggc ccc cct gac agc atg gct gcc tcg ccc tcc cca 6672
Pro Leu Ala Ser Gly Pro Pro Asp Ser Met Ala Ala Ser Pro Ser Pro
2210 2215 2220

aag aaa gat gtg ctg agt ctc tcc ggt tta tcc tct gac cca gca gac 6720
Lys Lys Asp Val Leu Ser Leu Ser Gly Leu Ser Ser Asp Pro Ala Asp
2225 2230 2235 2240

ctg gac ccc 6729
Leu Asp Pro

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Met Asp Glu Glu Glu Asp Gly Ala Gly Ala Glu Glu Ser Gly Gln Pro
1 5 10 15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag 96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
20 25 30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
35 40 45

gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg 192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
50 55 60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac 240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65 70 75 80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg 288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
85 90 95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag 336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
100 105 110

cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt 384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe

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        115                        120                        125

gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag      432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                     135                     140

aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc      480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                     150                     155                     160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc      528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                     170                     175

tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac      576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                     185                     190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg      624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                     200                     205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc      672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                     215                     220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg      720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                     230                     235                     240

tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag      768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                     250                     255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct      816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                     265                     270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg      864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                     280                     285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc      912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                     295                     300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat      960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                     310                     315                     320

acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac     1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                     330                     335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca     1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                     345                     350

ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc     1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                     360                     365

ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc     1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
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    370                 375                 380

ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag     1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc     1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc     1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc     1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg     1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc     1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac     1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc     1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg     1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg     1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac     1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca     1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act     1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg     1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                 600                 605

gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc     1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
    610                 615                 620

cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt     1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
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625                 630                 635                 640

acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag     1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                645                 650                 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg     2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca     2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
        675                 680                 685

gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac     2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat     2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                 710                 715                 720

gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca     2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725                 730                 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc     2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
            740                 745                 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag     2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
        755                 760                 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc     2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
    770                 775                 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc     2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                 790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg     2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805                 810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg     2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
            820                 825                 830

gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc     2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
        835                 840                 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac     2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
    850                 855                 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc     2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880

agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg     2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
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                885                 890                 895

gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg     2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
            900                 905                 910

gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa     2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
        915                 920                 925

gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac     2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
    930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg     2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
945                 950                 955                 960

gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag     2928
Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg     2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa     3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
        995                1000                1005

cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca     3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
   1010                1015                1020

cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg     3120
Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
1025               1030                1035                1040

ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga     3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
               1045                1050                1055

gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg     3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
           1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc     3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
       1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc     3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
   1090                1095                1100

ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat     3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105               1110                1115                1120

gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac     3408
Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
               1125                1130                1135

cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac     3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
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        1140                    1145                    1150

ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc      3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
        1155                    1160                    1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca      3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
    1170                    1175                    1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg      3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185                    1190                    1195                1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa      3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
                1205                    1210                    1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc      3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
            1220                    1225                    1230

tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt      3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
        1235                    1240                    1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc      3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
    1250                    1255                    1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac      3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265                    1270                    1275                1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc      3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
                1285                    1290                    1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc      3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
            1300                    1305                    1310

tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg      3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
        1315                    1320                    1325

gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg      4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
    1330                    1335                    1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg      4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345                    1350                    1355                1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga      4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
                1365                    1370                    1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc      4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
            1380                    1385                    1390

aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc      4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
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     1395                1400                1405

ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac    4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
    1410                1415                1420

acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga    4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
1425                1430                1435                1440

tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg    4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                1445                1450                1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat    4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
            1460                1465                1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac    4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
        1475                1480                1485

aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc    4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
    1490                1495                1500

ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat    4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1505                1510                1515                1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag    4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                1525                1530                1535

aag cga cta cgg agg ctg gag aaa aag aga agg agt aag gag aag cag    4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln
            1540                1545                1550

atg gcc gaa gcc cag tgc aag ccc tac tac tct gac tac tcg aga ttc    4704
Met Ala Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe
        1555                1560                1565

cgg ctc ctt gtc cac cac ctg tgt acc agc cac tac ctg gac ctc ttc    4752
Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe
    1570                1575                1580

atc act ggt gtc atc ggg ctg aac gtg gtc act atg gcc atg gaa cat    4800
Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met Glu His
1585                1590                1595                1600

tac cag cag ccc cag atc ctg gac gag gct ctg aag atc tgc aat tac    4848
Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr
                1605                1610                1615

atc ttt acc gtc atc ttt gtc ttt gag tca gtt ttc aaa ctt gtg gcc    4896
Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala
            1620                1625                1630

ttt ggc ttc cgc cgt ttc ttc cag gac agg tgg aac cag ctg gac ctg    4944
Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu
        1635                1640                1645

gct att gtg ctt ctg tcc atc atg ggc atc aca ctg gag gag att gag    4992
Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu
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1650 1655 1660

gtc aat ctg tcg ctg ccc atc aac ccc acc atc atc cgt atc atg agg 5040
Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg
1665 1670 1675 1680

gtg ctc cgc att gct cga gtt ctg aag ctg ttg aag atg gct gtg ggc 5088
Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly
1685 1690 1695

atg cgg gca ctg ctg cac acg gtg atg cag gcc ctg ccc cag gtg ggg 5136
Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln Val Gly
1700 1705 1710

aac ctg gga ctt ctc ttc atg tta ttg ttt ttc atc ttt gca gct ctg 5184
Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu
1715 1720 1725

ggc gtg gag ctc ttt gga gac ctg gag tgt gat gag aca cac cct tgt 5232
Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys
1730 1735 1740

gag ggc ttg ggt cgg cat gcc acc ttt agg aac ttt ggt atg gcc ttt 5280
Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe
1745 1750 1755 1760

ctg acc ctc ttc cga gtc tcc act ggt gac aac tgg aat ggt att atg 5328
Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met
1765 1770 1775

aag gac acc ctc cgg gac tgt gac cag gag tcc acc tgc tac aac act 5376
Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr
1780 1785 1790

gtc atc tcc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt 5424
Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe
1795 1800 1805

gtg ctg gtc aac gtg gtc ata gct gtg ctg atg aag cac ctg gaa gaa 5472
Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu Glu Glu
1810 1815 1820

agc aac aaa gag gcc aag gag gag gcc gag ctc gag gcc gag ctg gag 5520
Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu
1825 1830 1835 1840

ctg gag atg aag acg ctc agc ccg cag ccc cac tcc ccg ctg ggc agc 5568
Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser
1845 1850 1855

ccc ttc ctc tgg ccc ggg gtg gag ggt gtc aac agt act gac agc cct 5616
Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro
1860 1865 1870

aag cct ggg gct cca cac acc act gcc cac att gga gca gcc tcg ggc 5664
Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala Ser Gly
1875 1880 1885

ttc tcc ctt gag cac ccc acg atg gta ccc cac ccc gag gag gtg cca 5712
Phe Ser Leu Glu His Pro Thr Met Val Pro His Pro Glu Glu Val Pro
1890 1895 1900

gtc ccc cta gga cca gac ctg ctg act gtg agg aag tct ggt gtc agc 5760
Val Pro Leu Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser

1905 1910 1915 1920

cgg acg cac tct ctg ccc aat gac agc tac atg tgc cgc aat ggg agc 5808
Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg Asn Gly Ser
1925 1930 1935

act gct gag aga tcc cta gga cac agg ggc tgg ggg ctc ccc aaa gcc 5856
Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala
1940 1945 1950

cag tca ggc tcc atc ttg tcc gtt cac tcc caa cca gca gac acc agc 5904
Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser
1955 1960 1965

tgc atc cta cag ctt ccc aaa gat gtg cac tat ctg ctc cag cct cat 5952
Cys Ile Leu Gln Leu Pro Lys Asp Val His Tyr Leu Leu Gln Pro His
1970 1975 1980

ggg gct ccc acc tgg ggc gcc atc cct aaa cta ccc cca cct ggc cgc 6000
Gly Ala Pro Thr Trp Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg
1985 1990 1995 2000

tcc cct ctg gct cag agg cct ctc agg cgc cag gca gca ata agg act 6048
Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr
2005 2010 2015

gac tcc ctg gat gtg cag ggc ctg ggt agc cgg gaa gac ctg ttg tca 6096
Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser
2020 2025 2030

gag gtg agt ggg ccc tcc tgc cct ctg acc cgg tcc tca tcc ttc tgg 6144
Glu Val Ser Gly Pro Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp
2035 2040 2045

ggc ggg tcg agc atc cag gtg cag cag cgt tcc ggc atc cag agc aaa 6192
Gly Gly Ser Ser Ile Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys
2050 2055 2060

gtc tcc aag cac atc cgc ctg cca gcc cct tgc cca ggc ctg gaa ccc 6240
Val Ser Lys His Ile Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro
2065 2070 2075 2080

agc tgg gcc aag gac cct cca gag acc aga agc agc tta gag ctg gac 6288
Ser Trp Ala Lys Asp Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp
2085 2090 2095

acg gag ctg agc tgg att tca gga gac ctc ctt ccc agc agc cag gaa 6336
Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu
2100 2105 2110

gaa ccc ctg ttc cca cgg gac ctg aag aag tgc tac agt gta gag acc 6384
Glu Pro Leu Phe Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr
2115 2120 2125

cag agc tgc agg cgc agg cct ggg ttc tgg cta gat gaa cag cgg aga 6432
Gln Ser Cys Arg Arg Arg Pro Gly Phe Trp Leu Asp Glu Gln Arg Arg
2130 2135 2140

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His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu
2145 2150 2155 2160

tgt cca agc ccc tca agc ctc ggg ggc caa cct ctt ggg ggt cct ggg 6528
Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly

2165 2170 2175

agc cgg cct aag aaa aaa ctc agc cca ccc agt atc tct ata gac ccc 6576
Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro
2180 2185 2190

ccg gag agc cag ggc tct cgg ccc cca tgc agt cct ggt gtc tgc ctc 6624
Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu
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Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser
2210 2215 2220

ccc ctt gac agc acg gct gcc tca ccc tcc cca aag aaa gac acg ctg 6720
Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu
2225 2230 2235 2240

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Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
20 25 30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
35 40 45

gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg 192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
50 55 60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac 240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65 70 75 80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg 288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
85 90 95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag 336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
100 105 110

cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt 384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
115 120 125

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gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag    432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc    480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc    528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac    576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg    624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc    672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg    720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag    768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct    816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg    864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc    912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat    960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac   1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca   1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc   1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365

ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc   1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380
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ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag     1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc     1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc     1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc     1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg     1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc     1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac     1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc     1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg     1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg     1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac     1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca     1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act     1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg     1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                 600                 605

gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc     1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
    610                 615                 620

cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt     1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640
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acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag 1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
645 650 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg 2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
660 665 670

aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca 2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
675 680 685

gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac 2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
690 695 700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat 2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705 710 715 720

gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca 2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
725 730 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc 2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
740 745 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag 2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
755 760 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc 2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
770 775 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc 2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785 790 795 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg 2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
805 810 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg 2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
820 825 830

gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc 2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
835 840 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac 2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
850 855 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc 2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865 870 875 880

agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg 2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
885 890 895

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gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg   2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
            900                 905                 910

gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa   2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
        915                 920                 925

gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac   2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
    930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg   2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
945                 950                 955                 960

gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag   2928
Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg   2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa   3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
        995                 1000                1005

cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca   3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
    1010                1015                1020

cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg   3120
Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
1025                1030                1035                1040

ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga   3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                1045                1050                1055

gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg   3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
            1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc   3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
        1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc   3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
    1090                1095                1100

ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat   3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105                1110                1115                1120

gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac   3408
Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
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cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac   3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
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ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc 3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
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cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca 3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
1170 1175 1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg 3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185 1190 1195 1200

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Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
1205 1210 1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc 3696
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1220 1225 1230

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Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
1235 1240 1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc 3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
1250 1255 1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac 3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265 1270 1275 1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc 3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
1285 1290 1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc 3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
1300 1305 1310

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Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
1315 1320 1325

gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg 4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
1330 1335 1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg 4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345 1350 1355 1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga 4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
1365 1370 1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc 4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
1380 1385 1390

aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc 4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
1395 1400 1405

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ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac    4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
    1410                1415                1420

acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga    4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
1425                1430                1435                1440

tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg    4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                1445                1450                1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat    4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
            1460                1465                1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac    4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
        1475                1480                1485

aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc    4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
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ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat    4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1505                1510                1515                1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag    4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                1525                1530                1535

aag cga cta cgg agg ctg gag aaa aag aga agg aat cta atg ttg gac    4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Asn Leu Met Leu Asp
            1540                1545                1550

gat gta att gct tcc ggc agc tca gcc agc gct gcg tca gaa gcc cag    4704
Asp Val Ile Ala Ser Gly Ser Ser Ala Ser Ala Ala Ser Glu Ala Gln
        1555                1560                1565

tgc aag ccc tac tac tct gac tac tcg aga ttc cgg ctc ctt gtc cac    4752
Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His
    1570                1575                1580

cac ctg tgt acc agc cac tac ctg gac ctc ttc atc act ggt gtc atc    4800
His Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile
1585                1590                1595                1600

ggg ctg aac gtg gtc act atg gcc atg gaa cat tac cag cag ccc cag    4848
Gly Leu Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln
                1605                1610                1615

atc ctg gac gag gct ctg aag atc tgc aat tac atc ttt acc gtc atc    4896
Ile Leu Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile
            1620                1625                1630

ttt gtc ttt gag tca gtt ttc aaa ctt gtg gcc ttt ggc ttc cgc cgt    4944
Phe Val Phe Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg
        1635                1640                1645

ttc ttc cag gac agg tgg aac cag ctg gac ctg gct att gtg ctt ctg    4992
Phe Phe Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu
    1650                1655                1660
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tcc atc atg ggc atc aca ctg gag gag att gag gtc aac ctg tcg ctg 5040
Ser Ile Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Leu Ser Leu
1665 1670 1675 1680

ccc atc aac ccc acc atc atc cgt atc atg agg gtg ctc cgc att gct 5088
Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala
1685 1690 1695

cga gtt ctg aag ctg ttg aag atg gct gtg ggc atg cgg gca ctg ctg 5136
Arg Val Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu
1700 1705 1710

cac acg gtg atg cag gcc ctg ccc cag gtg ggg aac ctg gga ctt ctc 5184
His Thr Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu
1715 1720 1725

ttc atg tta ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt 5232
Phe Met Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe
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gga gac ctg gag tgt gat gag aca cac cct tgt gag ggc ttg ggt cgg 5280
Gly Asp Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg
1745 1750 1755 1760

cat gcc acc ttt agg aac ttt ggt atg gcc ttt ctg acc ctc ttc cga 5328
His Ala Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg
1765 1770 1775

gtc tcc act ggt gac aac tgg aat ggt att atg aag gac acc ctc cgg 5376
Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg
1780 1785 1790

gac tgt gac cag gag tcc acc tgc tac aac act gtc atc tcc cct atc 5424
Asp Cys Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile
1795 1800 1805

tac ttt gtg tcc ttc gtg ctg acg gcc cag ttt gtg ctg gtc aac gtg 5472
Tyr Phe Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val
1810 1815 1820

gtc ata gct gtg ctg atg aag cac ctg gaa gaa agc aac aaa gag gcc 5520
Val Ile Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala
1825 1830 1835 1840

aag gag gag gcc gag ctc gag gcc gag ctg gag ctg gag atg aag acg 5568
Lys Glu Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr
1845 1850 1855

ctc agc ccg cag ccc cac tcc ccg ctg ggc agc ccc ttc ctc tgg ccc 5616
Leu Ser Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro
1860 1865 1870

ggg gtg gag ggt gtc aac agt act gac agc cct aag cct ggg gct cca 5664
Gly Val Glu Gly Val Asn Ser Thr Asp Ser Pro Lys Pro Gly Ala Pro
1875 1880 1885

cac acc act gcc cac att gga gca gcc tcg ggc ttc tcc ctt gag cac 5712
His Thr Thr Ala His Ile Gly Ala Ala Ser Gly Phe Ser Leu Glu His
1890 1895 1900

ccc acg atg gta ccc cac ccc gag gag gtg cca gtc ccc cta gga cca 5760
Pro Thr Met Val Pro His Pro Glu Glu Val Pro Val Pro Leu Gly Pro
1905 1910 1915 1920

gac ctg ctg act gtg agg aag tct ggt gtc agc cgg acg cac tct ctg 5808
Asp Leu Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu
1925 1930 1935

ccc aat gac agc tac atg tgc cgc aat ggg agc act gct gag aga tcc 5856
Pro Asn Asp Ser Tyr Met Cys Arg Asn Gly Ser Thr Ala Glu Arg Ser
1940 1945 1950

cta gga cac agg ggc tgg ggg ctc ccc aaa gcc cag tca ggc tcc atc 5904
Leu Gly His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Ile
1955 1960 1965

ttg tcc gtt cac tcc caa cca gca gac acc agc tgc atc cta cag ctt 5952
Leu Ser Val His Ser Gln Pro Ala Asp Thr Ser Cys Ile Leu Gln Leu
1970 1975 1980

ccc aaa gat gtg cac tat ctg ctc cag cct cat ggg gct ccc acc tgg 6000
Pro Lys Asp Val His Tyr Leu Leu Gln Pro His Gly Ala Pro Thr Trp
1985 1990 1995 2000

ggc gcc atc cct aaa cta ccc cca cct ggc cgc tcc cct ctg gct cag 6048
Gly Ala Ile Pro Lys Leu Pro Pro Pro Gly Arg Ser Pro Leu Ala Gln
2005 2010 2015

agg cct ctc agg cgc cag gca gca ata agg act gac tcc ctg gat gtg 6096
Arg Pro Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val
2020 2025 2030

cag ggc ctg ggt agc cgg gaa gac ctg ttg tca gag gtg agt ggg ccc 6144
Gln Gly Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro
2035 2040 2045

tcc tgc cct ctg acc cgg tcc tca tcc ttc tgg ggc ggg tcg agc atc 6192
Ser Cys Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile
2050 2055 2060

cag gtg cag cag cgt tcc ggc atc cag agc aaa gtc tcc aag cac atc 6240
Gln Val Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile
2065 2070 2075 2080

cgc ctg cca gcc cct tgc cca ggc ctg gaa ccc agc tgg gcc aag gac 6288
Arg Leu Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp
2085 2090 2095

cct cca gag acc aga agc agc tta gag ctg gac acg gag ctg agc tgg 6336
Pro Pro Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp
2100 2105 2110

att tca gga gac ctc ctt ccc agc agc cag gaa gaa ccc ctg ttc cca 6384
Ile Ser Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro
2115 2120 2125

cgg gac ctg aag aag tgc tac agt gta gag acc cag agc tgc agg cgc 6432
Arg Asp Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg
2130 2135 2140

agg cct ggg ttc tgg cta gat gaa cag cgg aga cac tcc att gct gtc 6480
Arg Pro Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val
2145 2150 2155 2160

agc tgt ctg gac agc ggc tcc caa ccc cgc cta tgt cca agc ccc tca 6528
Ser Cys Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser
2165 2170 2175

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agc ctc ggg ggc caa cct ctt ggg ggt cct ggg agc cgg cct aag aaa      6576
Ser Leu Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys
            2180                2185                2190

aaa ctc agc cca ccc agt atc tct ata gac ccc ccg gag agc cag ggc      6624
Lys Leu Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly
        2195                2200                2205

tct cgg ccc cca tgc agt cct ggt gtc tgc ctc agg agg agg gcg ccg      6672
Ser Arg Pro Pro Cys Ser Pro Gly Val Cys Leu Arg Arg Arg Ala Pro
    2210                2215                2220

gcc agt gac tct aag gat ccc tcg gtc tcc agc ccc ctt gac agc acg      6720
Ala Ser Asp Ser Lys Asp Pro Ser Val Ser Ser Pro Leu Asp Ser Thr
2225                2230                2235                2240

gct gcc tca ccc tcc cca aag aaa gac acg ctg agt ctc tct ggt ttg      6768
Ala Ala Ser Pro Ser Pro Lys Lys Asp Thr Leu Ser Leu Ser Gly Leu
                2245                2250                2255

tct tct gac cca aca gac atg gac ccc                                  6795
Ser Ser Asp Pro Thr Asp Met Asp Pro
            2260                2265


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  1               5                  10                  15

cgt agc ttc acg cag ctc aac gac ctg tcc ggg gcc ggg ggc cgg cag      96
Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
             20                  25                  30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg      144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
         35                  40                  45

gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg      192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
     50                  55                  60

agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac      240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
 65                  70                  75                  80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg      288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
                 85                  90                  95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag      336
Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110
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cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt      384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag      432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc      480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc      528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac      576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg      624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc      672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg      720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag      768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct      816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg      864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc      912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat      960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac     1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca     1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
            340                 345                 350

ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc     1104
Leu Glu Gly Trp Val Asp Ile Met Tyr Phe Val Met Asp Ala His Ser
        355                 360                 365
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ttc tac aac ttc atc tac ttc att ctt ctc atc atc gtg ggc tcc ttc  1152
Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                 375                 380

ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag  1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                 390                 395                 400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc  1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                 410                 415

ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc  1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                 425                 430

tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc  1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                 440                 445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg  1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                 455                 460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc  1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                 470                 475                 480

agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac  1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                 490                 495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc  1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                 505                 510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg  1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                 520                 525

tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg  1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                 535                 540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac  1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                 550                 555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca  1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                 570                 575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act  1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                 585                 590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg  1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                 600                 605

gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc  1872
Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
    610                 615                 620
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cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt     1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625                 630                 635                 640

acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag     1968
Thr Gly Ala Cys His Ser Ser Cys Lys Ile Ser Ser Pro Cys Ser Lys
                645                 650                 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg     2016
Ala Asp Ser Gly Ala Cys Gly Pro Asp Ser Cys Pro Tyr Cys Ala Arg
            660                 665                 670

aca gga gca gga gag cca gag tcc gct gac cat gtc atg cct gac tca     2064
Thr Gly Ala Gly Glu Pro Glu Ser Ala Asp His Val Met Pro Asp Ser
        675                 680                 685

gac agc gag gct gtg tat gag ttc aca cag gac gct cag cac agt gac     2112
Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
    690                 695                 700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat     2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705                 710                 715                 720

gca gag cct agt tct gtg ctg gct ttc tgg agg ctg atc tgt gac aca     2208
Ala Glu Pro Ser Ser Val Leu Ala Phe Trp Arg Leu Ile Cys Asp Thr
                725                 730                 735

ttc cgg aag atc gta gat agc aaa tac ttt ggc cgg gga atc atg atc     2256
Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
            740                 745                 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag     2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
        755                 760                 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc     2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
    770                 775                 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc     2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785                 790                 795                 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg     2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
                805                 810                 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg     2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
            820                 825                 830

gtg ctg cgg acc ttc cgc ctg atg cgg gtg ctg aag ctg gtg cgc ttc     2544
Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
        835                 840                 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac     2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
    850                 855                 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc     2640
Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880
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agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg    2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
                885                 890                 895

gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg    2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
            900                 905                 910

gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa    2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
        915                 920                 925

gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac    2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
    930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg    2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
945                 950                 955                 960

gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag    2928
Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg    2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa    3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
        995                1000                1005

cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca    3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
   1010                1015                1020

cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg    3120
Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
1025               1030                1035                1040

ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga    3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
               1045                1050                1055

gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg    3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
           1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc    3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
       1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc    3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
   1090                1095                1100

ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat    3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105               1110                1115                1120

gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac    3408
Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
               1125                1130                1135
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cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac 3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
1140 1145 1150

ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc 3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
1155 1160 1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca 3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
1170 1175 1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg 3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185 1190 1195 1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa 3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
1205 1210 1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc 3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
1220 1225 1230

tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt 3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
1235 1240 1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc 3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
1250 1255 1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac 3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265 1270 1275 1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc 3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
1285 1290 1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc 3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
1300 1305 1310

tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg 3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
1315 1320 1325

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Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
1330 1335 1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg 4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345 1350 1355 1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga 4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
1365 1370 1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc 4176
Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
1380 1385 1390

aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc 4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
1395 1400 1405

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Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
1410 1415 1420

acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga 4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
1425 1430 1435 1440

tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg 4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
1445 1450 1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tac 4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
1460 1465 1470

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Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
1475 1480 1485

aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc 4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
1490 1495 1500

ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat 4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1505 1510 1515 1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag 4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
1525 1530 1535

aag cga cta cgg agg ctg gag aaa aag aga agg agt aag gag aag cag 4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Ser Lys Glu Lys Gln
1540 1545 1550

atg gcc gat cta atg ttg gac gat gta att gct tcc ggc agc tca gcc 4704
Met Ala Asp Leu Met Leu Asp Asp Val Ile Ala Ser Gly Ser Ser Ala
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agc gct gcg tca gaa gcc cag tgc aag ccc tac tac tct gac tac tcg 4752
Ser Ala Ala Ser Glu Ala Gln Cys Lys Pro Tyr Tyr Ser Asp Tyr Ser
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aga ttc cgg ctc ctt gtc cac cac ctg tgt acc agc cac tac ctg gac 4800
Arg Phe Arg Leu Leu Val His His Leu Cys Thr Ser His Tyr Leu Asp
1585 1590 1595 1600

ctc ttc atc act ggt gtc atc ggg ctg aac gtg gtc act atg gcc atg 4848
Leu Phe Ile Thr Gly Val Ile Gly Leu Asn Val Val Thr Met Ala Met
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gaa cat tac cag cag ccc cag atc ctg gac gag gct ctg aag atc tgc 4896
Glu His Tyr Gln Gln Pro Gln Ile Leu Asp Glu Ala Leu Lys Ile Cys
1620 1625 1630

aat tac atc ttt acc gtc atc ttt gtc ttt gag tca gtt ttc aaa ctt 4944
Asn Tyr Ile Phe Thr Val Ile Phe Val Phe Glu Ser Val Phe Lys Leu
1635 1640 1645

gtg gcc ttt ggc ttc cgc cgt ttc ttc cag gac agg tgg aac cag ctg 4992
Val Ala Phe Gly Phe Arg Arg Phe Phe Gln Asp Arg Trp Asn Gln Leu
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gac ctg gct att gtg ctt ctg tcc atc atg ggc atc aca ctg gag gag 5040
Asp Leu Ala Ile Val Leu Leu Ser Ile Met Gly Ile Thr Leu Glu Glu
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Ile Glu Val Asn Leu Ser Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile
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Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala
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Val Gly Met Arg Ala Leu Leu His Thr Val Met Gln Ala Leu Pro Gln
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Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Phe Ala
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gct ctg ggc gtg gag ctc ttt gga gac ctg gag tgt gat gag aca cac 5280
Ala Leu Gly Val Glu Leu Phe Gly Asp Leu Glu Cys Asp Glu Thr His
1745 1750 1755 1760

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Pro Cys Glu Gly Leu Gly Arg His Ala Thr Phe Arg Asn Phe Gly Met
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Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly
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Ile Met Lys Asp Thr Leu Arg Asp Cys Asp Gln Glu Ser Thr Cys Tyr
1795 1800 1805

aac act gtc atc tcc cct atc tac ttt gtg tcc ttc gtg ctg acg gcc 5472
Asn Thr Val Ile Ser Pro Ile Tyr Phe Val Ser Phe Val Leu Thr Ala
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cag ttt gtg ctg gtc aac gtg gtc ata gct gtg ctg atg aag cac ctg 5520
Gln Phe Val Leu Val Asn Val Val Ile Ala Val Leu Met Lys His Leu
1825 1830 1835 1840

gaa gaa agc aac aaa gag gcc aag gag gag gcc gag ctc gag gcc gag 5568
Glu Glu Ser Asn Lys Glu Ala Lys Glu Glu Ala Glu Leu Glu Ala Glu
1845 1850 1855

ctg gag ctg gag atg aag acg ctc agc ccg cag ccc cac tcc ccg ctg 5616
Leu Glu Leu Glu Met Lys Thr Leu Ser Pro Gln Pro His Ser Pro Leu
1860 1865 1870

ggc agc ccc ttc ctc tgg ccc ggg gtg gag ggt gtc aac agt act gac 5664
Gly Ser Pro Phe Leu Trp Pro Gly Val Glu Gly Val Asn Ser Thr Asp
1875 1880 1885

agc cct aag cct ggg gct cca cac acc act gcc cac att gga gca gcc 5712
Ser Pro Lys Pro Gly Ala Pro His Thr Thr Ala His Ile Gly Ala Ala
1890 1895 1900

tcg ggc ttc tcc ctt gag cac ccc acg atg gta ccc cac ccc gag gag 5760
Ser Gly Phe Ser Leu Glu His Pro Thr Met Val Pro His Pro Glu Glu
1905 1910 1915 1920

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Val Pro Val Pro Leu Gly Pro Asp Leu Leu Thr Val Arg Lys Ser Gly
1925 1930 1935

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Val Ser Arg Thr His Ser Leu Pro Asn Asp Ser Tyr Met Cys Arg Asn
1940 1945 1950

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Gly Ser Thr Ala Glu Arg Ser Leu Gly His Arg Gly Trp Gly Leu Pro
1955 1960 1965

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Lys Ala Gln Ser Gly Ser Ile Leu Ser Val His Ser Gln Pro Ala Asp
1970 1975 1980

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Thr Ser Cys Ile Leu Gln Leu Pro Lys Asp Val His Tyr Leu Leu Gln
1985 1990 1995 2000

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Pro His Gly Ala Pro Thr Trp Gly Ala Ile Pro Lys Leu Pro Pro Pro
2005 2010 2015

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Gly Arg Ser Pro Leu Ala Gln Arg Pro Leu Arg Arg Gln Ala Ala Ile
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Arg Thr Asp Ser Leu Asp Val Gln Gly Leu Gly Ser Arg Glu Asp Leu
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Leu Ser Glu Val Ser Gly Pro Ser Cys Pro Leu Thr Arg Ser Ser Ser
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Phe Trp Gly Gly Ser Ser Ile Gln Val Gln Gln Arg Ser Gly Ile Gln
2065 2070 2075 2080

agc aaa gtc tcc aag cac atc cgc ctg cca gcc cct tgc cca ggc ctg 6288
Ser Lys Val Ser Lys His Ile Arg Leu Pro Ala Pro Cys Pro Gly Leu
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Glu Pro Ser Trp Ala Lys Asp Pro Pro Glu Thr Arg Ser Ser Leu Glu
2100 2105 2110

ctg gac acg gag ctg agc tgg att tca gga gac ctc ctt ccc agc agc 6384
Leu Asp Thr Glu Leu Ser Trp Ile Ser Gly Asp Leu Leu Pro Ser Ser
2115 2120 2125

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Gln Glu Glu Pro Leu Phe Pro Arg Asp Leu Lys Lys Cys Tyr Ser Val
2130 2135 2140

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Glu Thr Gln Ser Cys Arg Arg Arg Pro Gly Phe Trp Leu Asp Glu Gln
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Arg Arg His Ser Ile Ala Val Ser Cys Leu Asp Ser Gly Ser Gln Pro
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Arg Leu Cys Pro Ser Pro Ser Ser Leu Gly Gly Gln Pro Leu Gly Gly
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Pro Gly Ser Arg Pro Lys Lys Lys Leu Ser Pro Pro Ser Ile Ser Ile
2195 2200 2205

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Asp Pro Pro Glu Ser Gln Gly Ser Arg Pro Pro Cys Ser Pro Gly Val
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Cys Leu Arg Arg Arg Ala Pro Ala Ser Asp Ser Lys Asp Pro Ser Val
2225 2230 2235 2240

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Ser Ser Pro Leu Asp Ser Thr Ala Ala Ser Pro Ser Pro Lys Lys Asp
2245 2250 2255

acg ctg agt ctc tct ggt ttg tct tct gac cca aca gac atg gac ccc 6816
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Arg Ser Phe Thr Gln Leu Asn Asp Leu Ser Gly Ala Gly Gly Arg Gln
20 25 30

ggg ccg ggg tcg acg gaa aag gac ccg ggc agc gcg gac tcc gag gcg 144
Gly Pro Gly Ser Thr Glu Lys Asp Pro Gly Ser Ala Asp Ser Glu Ala
35 40 45

gag ggg ctg ccg tac ccg gcg cta gcc ccg gtg gtt ttc ttc tac ttg 192
Glu Gly Leu Pro Tyr Pro Ala Leu Ala Pro Val Val Phe Phe Tyr Leu
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agc cag gac agc cgc ccg cgg agc tgg tgt ctc cgc acg gtc tgt aac 240
Ser Gln Asp Ser Arg Pro Arg Ser Trp Cys Leu Arg Thr Val Cys Asn
65 70 75 80

ccg tgg ttc gag cga gtc agt atg ctg gtc att ctt ctc aac tgt gtg 288
Pro Trp Phe Glu Arg Val Ser Met Leu Val Ile Leu Leu Asn Cys Val
85 90 95

act ctg ggt atg ttc agg ccg tgt gag gac att gcc tgt gac tcc cag 336

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Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Ile Ala Cys Asp Ser Gln
            100                 105                 110

cgc tgc cgg atc ctg cag gcc ttc gat gac ttc atc ttt gcc ttc ttt      384
Arg Cys Arg Ile Leu Gln Ala Phe Asp Asp Phe Ile Phe Ala Phe Phe
        115                 120                 125

gct gtg gaa atg gtg gtg aag atg gtg gcc ttg ggc atc ttt ggg aag      432
Ala Val Glu Met Val Val Lys Met Val Ala Leu Gly Ile Phe Gly Lys
    130                 135                 140

aaa tgt tac ctg gga gac act tgg aac cgg ctt gac ttt ttc att gtc      480
Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val
145                 150                 155                 160

att gca ggg atg ctg gag tat tcg ctg gac ctg cag aac gtc agc ttc      528
Ile Ala Gly Met Leu Glu Tyr Ser Leu Asp Leu Gln Asn Val Ser Phe
                165                 170                 175

tcc gca gtc agg aca gtc cgt gtg ctg cga ccg ctc agg gcc att aac      576
Ser Ala Val Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala Ile Asn
            180                 185                 190

cgg gtg ccc agc atg cgc att ctc gtc aca tta ctg ctg gac acc ttg      624
Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp Thr Leu
        195                 200                 205

cct atg ctg ggc aac gtc ctg ctg ctc tgt ttc ttc gtc ttt ttc atc      672
Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile
    210                 215                 220

ttt ggc atc gtg ggc gtc cag ctg tgg gca gga ctg ctt cgc aac cgg      720
Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg
225                 230                 235                 240

tgc ttc ctc ccc gag aac ttc agc ctc ccc ctg agc gtg gac ctg gag      768
Cys Phe Leu Pro Glu Asn Phe Ser Leu Pro Leu Ser Val Asp Leu Glu
                245                 250                 255

cct tat tac cag aca gag aat gag gac gag agc ccc ttc atc tgc tct      816
Pro Tyr Tyr Gln Thr Glu Asn Glu Asp Glu Ser Pro Phe Ile Cys Ser
            260                 265                 270

cag cct cgg gag aat ggc atg aga tcc tgc agg agt gtg ccc aca ctg      864
Gln Pro Arg Glu Asn Gly Met Arg Ser Cys Arg Ser Val Pro Thr Leu
        275                 280                 285

cgt ggg gaa ggc ggt ggt ggc cca ccc tgc agt ctg gac tat gag acc      912
Arg Gly Glu Gly Gly Gly Gly Pro Pro Cys Ser Leu Asp Tyr Glu Thr
    290                 295                 300

tat aac agt tcc agc aac acc acc tgt gtc aac tgg aac cag tac tat      960
Tyr Asn Ser Ser Ser Asn Thr Thr Cys Val Asn Trp Asn Gln Tyr Tyr
305                 310                 315                 320

acc aac tgc tct gcg ggc gag cac aac ccc ttc aaa ggc gcc atc aac     1008
Thr Asn Cys Ser Ala Gly Glu His Asn Pro Phe Lys Gly Ala Ile Asn
                325                 330                 335

ttt gac aac att ggc tat gcc tgg atc gcc atc ttc cag gtc atc aca     1056
Phe Asp Asn Ile Gly Tyr Ala Trp Ile Ala Ile Phe Gln Val Ile Thr
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ctg gag ggc tgg gtc gac atc atg tac ttc gta atg gac gct cac tcc     1104
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Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser Phe
    370                     375                     380

ttc atg atc aac ctg tgc ctg gtg gtg att gcc acg cag ttc tcc gag     1200
Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser Glu
385                     390                     395                 400

acc aaa cag cgg gag agt cag ctg atg cgg gag cag cgt gta cga ttc     1248
Thr Lys Gln Arg Glu Ser Gln Leu Met Arg Glu Gln Arg Val Arg Phe
                405                     410                     415

ctg tcc aat gct agc acc ctg gca agc ttc tct gag cca ggc agc tgc     1296
Leu Ser Asn Ala Ser Thr Leu Ala Ser Phe Ser Glu Pro Gly Ser Cys
            420                     425                     430

tat gag gag cta ctc aag tac ctg gtg tac atc ctc cga aaa gca gcc     1344
Tyr Glu Glu Leu Leu Lys Tyr Leu Val Tyr Ile Leu Arg Lys Ala Ala
        435                     440                     445

cga agg ctg gcc cag gtc tct agg gct ata ggc gtg cgg gct ggg ctg     1392
Arg Arg Leu Ala Gln Val Ser Arg Ala Ile Gly Val Arg Ala Gly Leu
    450                     455                     460

ctc agc agc cca gtg gcc cgt agt ggg cag gag ccc cag ccc agt ggc     1440
Leu Ser Ser Pro Val Ala Arg Ser Gly Gln Glu Pro Gln Pro Ser Gly
465                     470                     475                 480

agc tgc act cgc tca cac cgt cgt ctg tct gtc cac cac ctg gtc cac     1488
Ser Cys Thr Arg Ser His Arg Arg Leu Ser Val His His Leu Val His
                485                     490                     495

cac cat cac cac cac cat cac cac tac cac ctg ggt aat ggg acg ctc     1536
His His His His His His His His Tyr His Leu Gly Asn Gly Thr Leu
            500                     505                     510

aga gtt ccc cgg gcc agc cca gag atc cag gac agg gat gcc aat ggg     1584
Arg Val Pro Arg Ala Ser Pro Glu Ile Gln Asp Arg Asp Ala Asn Gly
        515                     520                     525

tct cgc cgg ctc atg cta cca cca ccc tct aca ccc act ccc tct ggg     1632
Ser Arg Arg Leu Met Leu Pro Pro Pro Ser Thr Pro Thr Pro Ser Gly
    530                     535                     540

ggc cct ccg agg ggt gcg gag tct gta cac agc ttc tac cat gct gac     1680
Gly Pro Pro Arg Gly Ala Glu Ser Val His Ser Phe Tyr His Ala Asp
545                     550                     555                 560

tgc cac ttg gag cca gtc cgt tgc cag gca ccc cct ccc aga tgc cca     1728
Cys His Leu Glu Pro Val Arg Cys Gln Ala Pro Pro Pro Arg Cys Pro
                565                     570                     575

tcg gag gca tct ggt agg act gtg ggt agt ggg aag gtg tac ccc act     1776
Ser Glu Ala Ser Gly Arg Thr Val Gly Ser Gly Lys Val Tyr Pro Thr
            580                     585                     590

gtg cat acc agc cct cca cca gag ata ctg aag gat aaa gca cta gtg     1824
Val His Thr Ser Pro Pro Pro Glu Ile Leu Lys Asp Lys Ala Leu Val
        595                     600                     605

gag gtg gcc ccc agc cct ggg ccc ccc acc ctc acc agc ttc aac atc     1872
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Glu Val Ala Pro Ser Pro Gly Pro Pro Thr Leu Thr Ser Phe Asn Ile
610 615 620

cca cct ggg ccc ttc agc tcc atg cac aag ctc ctg gag aca cag agt 1920
Pro Pro Gly Pro Phe Ser Ser Met His Lys Leu Leu Glu Thr Gln Ser
625 630 635 640

acg gga gcc tgc cat agc tcc tgc aaa atc tcc agc cct tgc tcc aag 1968
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645 650 655

gca gac agt gga gcc tgc ggg ccg gac agt tgt ccc tac tgt gcc cgg 2016
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660 665 670

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675 680 685

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Asp Ser Glu Ala Val Tyr Glu Phe Thr Gln Asp Ala Gln His Ser Asp
690 695 700

ctc cgg gat ccc cac agc cgg cgg cga cag cgg agc ctg ggc cca gat 2160
Leu Arg Asp Pro His Ser Arg Arg Arg Gln Arg Ser Leu Gly Pro Asp
705 710 715 720

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725 730 735

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Phe Arg Lys Ile Val Asp Ser Lys Tyr Phe Gly Arg Gly Ile Met Ile
740 745 750

gcc atc ctg gtc aat aca ctc agc atg ggc atc gag tac cac gag cag 2304
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Ile Glu Tyr His Glu Gln
755 760 765

ccc gag gag ctc acc aac gcc ctg gaa atc agc aac atc gtc ttc acc 2352
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
770 775 780

agc ctc ttc gcc ttg gag atg ctg ctg aaa ctg ctt gtc tac ggt ccc 2400
Ser Leu Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Val Tyr Gly Pro
785 790 795 800

ttt ggc tac att aag aat ccc tac aac atc ttt gat ggt gtc att gtg 2448
Phe Gly Tyr Ile Lys Asn Pro Tyr Asn Ile Phe Asp Gly Val Ile Val
805 810 815

gtc atc agt gtg tgg gag att gtg ggc cag cag gga ggt ggc ctg tcg 2496
Val Ile Ser Val Trp Glu Ile Val Gly Gln Gln Gly Gly Gly Leu Ser
820 825 830

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Val Leu Arg Thr Phe Arg Leu Met Arg Val Leu Lys Leu Val Arg Phe
835 840 845

ctg ccg gcc ctg cag cgc cag ctc gtg gtg ctc atg aag acc atg gac 2592
Leu Pro Ala Leu Gln Arg Gln Leu Val Val Leu Met Lys Thr Met Asp
850 855 860

aac gtg gcc acc ttc tgc atg ctc ctc atg ctg ttc atc ttc atc ttc 2640

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Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe
865                 870                 875                 880

agc atc ctg ggc atg cat ctc ttt ggt tgc aag ttc gca tct gaa cgg     2688
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ala Ser Glu Arg
                885                 890                 895

gat ggg gac acg ttg cca gac cgg aag aat ttc gac tcc ctg ctc tgg     2736
Asp Gly Asp Thr Leu Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp
            900                 905                 910

gcc atc gtc act gtc ttt cag att ctg act cag gaa gac tgg aat aaa     2784
Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn Lys
        915                 920                 925

gtc ctc tac aac ggc atg gcc tcc aca tcg tct tgg gct gct ctt tac     2832
Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu Tyr
    930                 935                 940

ttc atc gcc ctc atg act ttt ggc aac tat gtg ctc ttt aac ctg ctg     2880
Phe Ile Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu Leu
945                 950                 955                 960

gtg gcc att ctt gtg gaa gga ttc cag gca gag gga gat gcc acc aag     2928
Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Thr Lys
                965                 970                 975

tct gag tca gag cct gat ttc ttt tcg ccc agt gtg gat ggt gat ggg     2976
Ser Glu Ser Glu Pro Asp Phe Phe Ser Pro Ser Val Asp Gly Asp Gly
            980                 985                 990

gac aga aag aag cgc ttg gcc ctg gtg gct ttg gga gaa cac gcg gaa     3024
Asp Arg Lys Lys Arg Leu Ala Leu Val Ala Leu Gly Glu His Ala Glu
        995                 1000                1005

cta cga aag agc ctt ttg cca ccc ctc atc atc cat acg gct gcg aca     3072
Leu Arg Lys Ser Leu Leu Pro Pro Leu Ile Ile His Thr Ala Ala Thr
    1010                1015                1020

cca atg tca cac ccc aag agc tcc agc aca ggt gtg ggg gaa gca ctg     3120
Pro Met Ser His Pro Lys Ser Ser Ser Thr Gly Val Gly Glu Ala Leu
1025                1030                1035                1040

ggc tct ggc tct cga cgt acc agt agc agt ggg tcc gct gag cct gga     3168
Gly Ser Gly Ser Arg Arg Thr Ser Ser Ser Gly Ser Ala Glu Pro Gly
                1045                1050                1055

gct gcc cac cat gag atg aaa tgt ccg cca agt gcc cgc agc tcc ccg     3216
Ala Ala His His Glu Met Lys Cys Pro Pro Ser Ala Arg Ser Ser Pro
            1060                1065                1070

cac agt ccc tgg agt gcg gca agc agc tgg acc agc agg cgc tcc agc     3264
His Ser Pro Trp Ser Ala Ala Ser Ser Trp Thr Ser Arg Arg Ser Ser
        1075                1080                1085

agg aac agc ctg ggc cgg gcc ccc agc cta aag cgg agg agc ccg agc     3312
Arg Asn Ser Leu Gly Arg Ala Pro Ser Leu Lys Arg Arg Ser Pro Ser
    1090                1095                1100

ggg gag cgg agg tcc ctg ctg tct gga gag ggc cag gag agt cag gat     3360
Gly Glu Arg Arg Ser Leu Leu Ser Gly Glu Gly Gln Glu Ser Gln Asp
1105                1110                1115                1120

gag gag gaa agt tca gaa gag gac cgg gcc agc cca gca ggc agt gac     3408
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Glu Glu Glu Ser Ser Glu Glu Asp Arg Ala Ser Pro Ala Gly Ser Asp
            1125                    1130                    1135

cat cgc cac agg ggt tcc ttg gaa cgt gag gcc aag agt tcc ttt gac    3456
His Arg His Arg Gly Ser Leu Glu Arg Glu Ala Lys Ser Ser Phe Asp
        1140                    1145                    1150

ctg cct gac act ctg cag gtg ccg ggg ctg cac cgc aca gcc agc ggc    3504
Leu Pro Asp Thr Leu Gln Val Pro Gly Leu His Arg Thr Ala Ser Gly
    1155                    1160                    1165

cgg agc tct gcc tct gag cac caa gac tgt aat ggc aag tcg gct tca    3552
Arg Ser Ser Ala Ser Glu His Gln Asp Cys Asn Gly Lys Ser Ala Ser
1170                    1175                    1180

ggg cgt ttg gcc cgc acc ctg agg act gat gac ccc caa ctg gat ggg    3600
Gly Arg Leu Ala Arg Thr Leu Arg Thr Asp Asp Pro Gln Leu Asp Gly
1185                1190                    1195                1200

gat gat gac aat gat gag gga aat ctg agc aaa ggg gaa cgc ata caa    3648
Asp Asp Asp Asn Asp Glu Gly Asn Leu Ser Lys Gly Glu Arg Ile Gln
            1205                    1210                    1215

gcc tgg gtc aga tcc cgg ctt cct gcc tgt tgc cga gag cga gat tcc    3696
Ala Trp Val Arg Ser Arg Leu Pro Ala Cys Cys Arg Glu Arg Asp Ser
        1220                    1225                    1230

tgg tcg gcc tat atc ttt cct cct cag tca agg ttt cgt ctc ctg tgt    3744
Trp Ser Ala Tyr Ile Phe Pro Pro Gln Ser Arg Phe Arg Leu Leu Cys
    1235                    1240                    1245

cac cgg atc atc acc cac aag atg ttt gac cat gtg gtc ctc gtc atc    3792
His Arg Ile Ile Thr His Lys Met Phe Asp His Val Val Leu Val Ile
1250                    1255                    1260

atc ttc ctc aac tgt atc acc atc gct atg gag cgc ccc aaa att gac    3840
Ile Phe Leu Asn Cys Ile Thr Ile Ala Met Glu Arg Pro Lys Ile Asp
1265                1270                    1275                1280

ccc cac agc gct gag cgc atc ttc ctg acc ctc tcc aac tac atc ttc    3888
Pro His Ser Ala Glu Arg Ile Phe Leu Thr Leu Ser Asn Tyr Ile Phe
            1285                    1290                    1295

acg gca gtc ttt cta gct gaa atg aca gtg aag gtg gtg gca ctg ggc    3936
Thr Ala Val Phe Leu Ala Glu Met Thr Val Lys Val Val Ala Leu Gly
        1300                    1305                    1310

tgg tgc ttt ggg gag cag gcc tac ctg cgc agc agc tgg aat gtg ctg    3984
Trp Cys Phe Gly Glu Gln Ala Tyr Leu Arg Ser Ser Trp Asn Val Leu
    1315                    1320                    1325

gac ggc ttg ctg gtg ctc atc tcc gtc atc gac atc ctg gtc tcc atg    4032
Asp Gly Leu Leu Val Leu Ile Ser Val Ile Asp Ile Leu Val Ser Met
1330                    1335                    1340

gtc tcc gac agc ggc acc aag atc ctt ggc atg ctg agg gtg ctg cgg    4080
Val Ser Asp Ser Gly Thr Lys Ile Leu Gly Met Leu Arg Val Leu Arg
1345                1350                    1355                1360

ctg ctg cgg acc ctg cgt cca ctc agg gtc atc agc cgg gcc cag gga    4128
Leu Leu Arg Thr Leu Arg Pro Leu Arg Val Ile Ser Arg Ala Gln Gly
            1365                    1370                    1375

ctg aag ctg gtg gta gag act ctg atg tca tcc ctc aaa ccc att ggc    4176
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Leu Lys Leu Val Val Glu Thr Leu Met Ser Ser Leu Lys Pro Ile Gly
            1380                1385                1390

aac att gtg gtc att tgc tgt gcc ttc ttc atc att ttt gga att ctc    4224
Asn Ile Val Val Ile Cys Cys Ala Phe Phe Ile Ile Phe Gly Ile Leu
        1395                1400                1405

ggg gtg cag ctc ttc aaa ggg aag ttc ttc gtg tgt cag ggt gag gac    4272
Gly Val Gln Leu Phe Lys Gly Lys Phe Phe Val Cys Gln Gly Glu Asp
    1410                1415                1420

acc agg aac atc act aac aaa tcc gac tgc gct gag gcc agc tac cga    4320
Thr Arg Asn Ile Thr Asn Lys Ser Asp Cys Ala Glu Ala Ser Tyr Arg
1425                1430                1435                1440

tgg gtc cgg cac aag tac aac ttt gac aac ctg ggc cag gct ctg atg    4368
Trp Val Arg His Lys Tyr Asn Phe Asp Asn Leu Gly Gln Ala Leu Met
                1445                1450                1455

tcc ctg ttt gtg ctg gcc tcc aag gat ggt tgg gtt gac atc atg tat    4416
Ser Leu Phe Val Leu Ala Ser Lys Asp Gly Trp Val Asp Ile Met Tyr
            1460                1465                1470

gat ggg ctg gat gct gtg ggt gtg gat cag cag ccc atc atg aac cac    4464
Asp Gly Leu Asp Ala Val Gly Val Asp Gln Gln Pro Ile Met Asn His
        1475                1480                1485

aac ccc tgg atg ctg cta tac ttc atc tcc ttc ctc ctc atc gtg gcc    4512
Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser Phe Leu Leu Ile Val Ala
    1490                1495                1500

ttc ttt gtc ctg aac atg ttt gtg ggc gtg gtg gtg gag aac ttc cat    4560
Phe Phe Val Leu Asn Met Phe Val Gly Val Val Val Glu Asn Phe His
1505                1510                1515                1520

aag tgc aga cag cac cag gag gag gag gag gcg agg cgg cgt gag gag    4608
Lys Cys Arg Gln His Gln Glu Glu Glu Glu Ala Arg Arg Arg Glu Glu
                1525                1530                1535

aag cga cta cgg agg ctg gag aaa aag aga agg aaa gcc cag tgc aag    4656
Lys Arg Leu Arg Arg Leu Glu Lys Lys Arg Arg Lys Ala Gln Cys Lys
            1540                1545                1550

ccc tac tac tct gac tac tcg aga ttc cgg ctc ctt gtc cac cac ctg    4704
Pro Tyr Tyr Ser Asp Tyr Ser Arg Phe Arg Leu Leu Val His His Leu
        1555                1560                1565

tgt acc agc cac tac ctg gac ctc ttc atc act ggt gtc atc ggg ctg    4752
Cys Thr Ser His Tyr Leu Asp Leu Phe Ile Thr Gly Val Ile Gly Leu
    1570                1575                1580

aac gtg gtc act atg gcc atg gaa cat tac cag cag ccc cag atc ctg    4800
Asn Val Val Thr Met Ala Met Glu His Tyr Gln Gln Pro Gln Ile Leu
1585                1590                1595                1600

gac gag gct ctg aag atc tgc aat tac atc ttt acc gtc atc ttt gtc    4848
Asp Glu Ala Leu Lys Ile Cys Asn Tyr Ile Phe Thr Val Ile Phe Val
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ttt gag tca gtt ttc aaa ctt gtg gcc ttt ggc ttc cgc cgt ttc ttc    4896
Phe Glu Ser Val Phe Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe
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Gln Asp Arg Trp Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Ile
1635 1640 1645

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Met Gly Ile Thr Leu Glu Glu Ile Glu Val Asn Leu Ser Leu Pro Ile
1650 1655 1660

aac ccc acc atc atc cgt atc atg agg gtg ctc cgc att gct cga gtt 5040
Asn Pro Thr Ile Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val
1665 1670 1675 1680

ctg aag ctg ttg aag atg gct gtg ggc atg cgg gca ctg ctg cac acg 5088
Leu Lys Leu Leu Lys Met Ala Val Gly Met Arg Ala Leu Leu His Thr
1685 1690 1695

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Val Met Gln Ala Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met
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tta ttg ttt ttc atc ttt gca gct ctg ggc gtg gag ctc ttt gga gac 5184
Leu Leu Phe Phe Ile Phe Ala Ala Leu Gly Val Glu Leu Phe Gly Asp
1715 1720 1725

ctg gag tgt gat gag aca cac cct tgt gag ggc ttg ggt cgg cat gcc 5232
Leu Glu Cys Asp Glu Thr His Pro Cys Glu Gly Leu Gly Arg His Ala
1730 1735 1740

acc ttt agg aac ttt ggt atg gcc ttt ctg acc ctc ttc cga gtc tcc 5280
Thr Phe Arg Asn Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser
1745 1750 1755 1760

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Thr Gly Asp Asn Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Asp Cys
1765 1770 1775

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Asp Gln Glu Ser Thr Cys Tyr Asn Thr Val Ile Ser Pro Ile Tyr Phe
1780 1785 1790

gtg tcc ttc gtg ctg acg gcc cag ttt gtg ctg gtc aac gtg gtc ata 5424
Val Ser Phe Val Leu Thr Ala Gln Phe Val Leu Val Asn Val Val Ile
1795 1800 1805

gct gtg ctg atg aag cac ctg gaa gaa agc aac aaa gag gcc aag gag 5472
Ala Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Lys Glu
1810 1815 1820

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Glu Ala Glu Leu Glu Ala Glu Leu Glu Leu Glu Met Lys Thr Leu Ser
1825 1830 1835 1840

ccg cag ccc cac tcc ccg ctg ggc agc ccc ttc ctc tgg ccc ggg gtg 5568
Pro Gln Pro His Ser Pro Leu Gly Ser Pro Phe Leu Trp Pro Gly Val
1845 1850 1855

gag ggt gtc aac agt act gac agc cct aag cct ggg gct cca cac acc 5616
Glu Gly Val Asn Ser Thr Asp Ser Pro Lys Pro Gly Ala Pro His Thr
1860 1865 1870

act gcc cac att gga gca gcc tcg ggc ttc tcc ctt gag cac ccc acg 5664
Thr Ala His Ile Gly Ala Ala Ser Gly Phe Ser Leu Glu His Pro Thr
1875 1880 1885

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Met Val Pro His Pro Glu Glu Val Pro Val Pro Leu Gly Pro Asp Leu
1890 1895 1900

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Leu Thr Val Arg Lys Ser Gly Val Ser Arg Thr His Ser Leu Pro Asn
1905 1910 1915 1920

gac agc tac atg tgc cgc aat ggg agc act gct gag aga tcc cta gga 5808
Asp Ser Tyr Met Cys Arg Asn Gly Ser Thr Ala Glu Arg Ser Leu Gly
1925 1930 1935

cac agg ggc tgg ggg ctc ccc aaa gcc cag tca ggc tcc atc ttg tcc 5856
His Arg Gly Trp Gly Leu Pro Lys Ala Gln Ser Gly Ser Ile Leu Ser
1940 1945 1950

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Val His Ser Gln Pro Ala Asp Thr Ser Cys Ile Leu Gln Leu Pro Lys
1955 1960 1965

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Asp Val His Tyr Leu Leu Gln Pro His Gly Ala Pro Thr Trp Gly Ala
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2005 2010 2015

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Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile Arg Leu
2050 2055 2060

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Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp Pro Pro
2065 2070 2075 2080

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Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser
2085 2090 2095

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Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro Arg Asp
2100 2105 2110

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Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg Arg Pro
2115 2120 2125

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Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys
2130 2135 2140

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Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser Ser Leu
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Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Gly Val Pro Gly Glu Pro
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Arg Gly Ala Gly Thr Arg Gly Gly Gly Gly Phe Glu Leu Gly Val Ser
35 40 45

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Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp
50 55 60

gag gag cag cgc gtc ccg tac ccg gcc ttg gcg gcc acg gtc ttc ttc 240
Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe Phe
65 70 75 80

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Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu Val
85 90 95

tgc aac cca tgg ttc gag cac gtg agc atg ctg gta atc atg ctc aac 336
Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu Asn

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            100                     105                     110

tgc gtg acc ctg ggc atg ttc cgg ccc tgt gag gac gtt gag tgc ggc      384
Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Val Glu Cys Gly
        115                 120                 125

tcc gag cgc tgc aac atc ctg gag gcc ttt gac gcc ttc att ttc gcc      432
Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe Ala
    130                 135                 140

ttt ttt gcg gtg gag atg gtc atc aag atg gtg gcc ttg ggg ctg ttc      480
Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu Phe
145                 150                 155                 160

ggg cag aag tgt tac ctg ggt gac acg tgg aac agg ctg gat ttc ttc      528
Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe
                165                 170                 175

atc gtc gtg gcg ggc atg atg gag tac tcg ttg gac gga cac aac gtg      576
Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn Val
            180                 185                 190

agc ctc tcg gct atc agg acc gtg cgg gtg ctg cgg ccc ctc cgc gcc      624
Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala
        195                 200                 205

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Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp
    210                 215                 220

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Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe
225                 230                 235                 240

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Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg
                245                 250                 255

aac cgc tgc ttc ctg gac agt gcc ttt gtc agg aac aac aac ctg acc      816
Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu Thr
            260                 265                 270

ttc ctg cgg ccg tac tac cag acg gag gag ggc gag gag aac ccg ttc      864
Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro Phe
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Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His Ile
    290                 295                 300

ccc ggc cgc cgc gac gtg cgc atg ccc tgc acc ctg ggc tgg gag gcc      960
Pro Gly Arg Arg Asp Val Arg Met Pro Cys Thr Leu Gly Trp Glu Ala
305                 310                 315                 320

tac acg cag ccg cag gcc gag ggg gtg ggc gct gca cgc aac gcc tgc     1008
Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala Cys
                325                 330                 335

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Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser Asn
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Pro His Asn Gly Ala Ile Asn Phe Asp Asn Thr Cys Tyr Ala Trp Ile
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Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu
385                 390                 395                 400

ctc atc atc gtg ggc tcc ttc ttc atg atc aac ctg tgc ctg gtg gtg    1248
Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
                405                 410                 415

att gcc acg cag ttc tcg gag acg aag cag cgg gag agt cag ctg atg    1296
Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met
            420                 425                 430

cgg gag cag cgg gca cgc cac ctg tcc aac gac agc acg ctg gcc agc    1344
Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala Ser
        435                 440                 445

ttc tcc gag cct ggc agc tgc tac gaa gag ctg ctg aag tac gtg ggc    1392
Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val Gly
    450                 455                 460

cac ata ttc cgc aag gtc aag cgg cgc agc ttg cgc ctc tac gcc cgc    1440
His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala Arg
465                 470                 475                 480

tgg cag agc cgc tgg cgc aag aag gtg gac ccc agt gct gtg caa ggc    1488
Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln Gly
                485                 490                 495

cag ggt ccc ggg cac cgc cag cgc cgg gca ggc agg cac aca gcc tcg    1536
Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala Ser
            500                 505                 510

gtg cac cac ctg gtc tac cac cac cat cac cac cac cac cac cac tac    1584
Val His His Leu Val Tyr His His His His His His His His His Tyr
        515                 520                 525

cat ttc agc cat ggc agc ccc cgc agg ccc ggc ccc gag cca ggc gcc    1632
His Phe Ser His Gly Ser Pro Arg Arg Pro Gly Pro Glu Pro Gly Ala
    530                 535                 540

tgc gac acc agg ctg gtc cga gct ggc gcg ccc ccc tcg cca cct tcc    1680
Cys Asp Thr Arg Leu Val Arg Ala Gly Ala Pro Pro Ser Pro Pro Ser
545                 550                 555                 560

cca ggc cgc gga ccc ccc gac gca gag tct gtg cac agc atc tac cat    1728
Pro Gly Arg Gly Pro Pro Asp Ala Glu Ser Val His Ser Ile Tyr His
                565                 570                 575

gcc gac tgc cac ata gag ggg ccg cag gag agg gcc cgg gtg ggc aca    1776
Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr
            580                 585                 590

tgc cgc agc cac tgc cgc tgc cag cct cag gct ggc cac agg gct ggg    1824
Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly
        595                 600                 605

cac cat gaa cta ccc cac gat cct gcc ctc agg ggt ggg cag cgg caa    1872
His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln
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610                    615                    620

agg cag cac cag ccc cgg acc caa ggg gaa gtg ggc cgg tgg acc gcc    1920
Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Ala
625                 630                 635                 640

agg cac cgg ggg cac ggc ccg ttg agc ttg aac agc cct gat ccc tac    1968
Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr
            645                 650                 655

gag aag atc ccg cat gtg gcc ggg gag cat gga ctg ggc caa gcc cct    2016
Glu Lys Ile Pro His Val Ala Gly Glu His Gly Leu Gly Gln Ala Pro
        660                 665                 670

ggc cat ctg tcg ggc ctc agt gtg ccc tgc ccc ctg ccc agc ccc cca    2064
Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro
    675                 680                 685

gcg ggc aca ctg acc tgt gag ctg aag agc tgc ccg tac tgc acc cgt    2112
Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg
690                 695                 700

gcc ctg gag gac ccg gag ggt gag ctc agc ggc tcg gaa agt gga gac    2160
Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp
705                 710                 715                 720

tca gat ggc cgt ggc gtc tat gaa ttc acg cag gac gtc cgg cac ggt    2208
Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly
                725                 730                 735

gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac aca cca ggc    2256
Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly
            740                 745                 750

cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca gcc ccg    2304
Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro
        755                 760                 765

ggc gag cca ggc tgg atg ggc cgc ctc tgg gtt acc ttc agc ggc aag    2352
Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys
    770                 775                 780

ctg cgc cgc atc gtg gac agc aag tac ttc agc cgt ggc atc atg atg    2400
Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met
785                 790                 795                 800

gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag    2448
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln
                805                 810                 815

ccc gag gag ctg act aat gct ctg gag atc agc aac atc gtg ttc acc    2496
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
            820                 825                 830

agc atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgc ggg cct    2544
Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro
        835                 840                 845

ctg ggc tac atc cgg aac ccg tac aac atc ttc gac ggc atc atc gtg    2592
Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val
    850                 855                 860

gtc atc agc gtc tgg gag atc gtg ggg cag gcg gac ggt ggc ttg tct    2640
Val Ile Ser Val Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser
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865 870 875 880

gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttt 2688
Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe
885 890 895

ctg cca gcc ctg cgg cgc cag ctc gtg gtg ctg gtg aag acc atg gac 2736
Leu Pro Ala Leu Arg Arg Gln Leu Val Val Leu Val Lys Thr Met Asp
900 905 910

aac gtg gct acc ttc tgc acg ctg ctc atg ctc ttc att ttc atc ttc 2784
Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe
915 920 925

agc atc ctg ggc atg cac ctt ttc ggc tgc aag ttc agc ctg aag aca 2832
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ser Leu Lys Thr
930 935 940

gac acc gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg 2880
Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu
945 950 955 960

tgg gcc atc gtc acc gtg ttc cag atc ctg acc cag gag gac tgg aac 2928
Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn
965 970 975

gtg gtc ctg tac aac ggc atg gcc tcc acc tcc tcc tgg gcc gcc ctc 2976
Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu
980 985 990

tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg 3024
Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu
995 1000 1005

ctg gtg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc gat gcc aac 3072
Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn
1010 1015 1020

aga tcc gac acg gac gag gac aag acg tcg gtc cac ttc gag gag gac 3120
Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp
1025 1030 1035 1040

ttc cac aag ctc aga gaa ctc cag acc aca gag ctg aag atg tgt tcc 3168
Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser
1045 1050 1055

ctg gcc gtg acc ccc aac ggc acc tgg agg gac gag gca gcc tgt ccc 3216
Leu Ala Val Thr Pro Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro
1060 1065 1070

ctc ccc tca tca tgt gca cag ctg cca cgc cca tgc cta ccc cca aga 3264
Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg
1075 1080 1085

gct cac cat tcc tgg atg cag ccc cca gcc tcc cag act ctc ggc gtg 3312
Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val
1090 1095 1100

gca gca gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctc cgg 3360
Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg
1105 1110 1115 1120

cag cct ccg aag ttc tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg 3408
Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp

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            1125                1130                1135

agc agc cgg cgc tcc agc tgg agc agc ctg ggc cgt gcc cag cct caa   3456
Ser Ser Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln
        1140                1145                1150

gcg ccg gcg tgc cag tgt ggg gaa cgt gag tcc ctg ctg tct ggc gag   3504
Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu
    1155                1160                1165

ggc aag ggc agc acc gac gac gaa gct gag gac ggc agg gcg cgc tcc   3552
Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser
    1170                1175                1180

ggg ccc cgt gcc acc cca ctg cgg cgg gcc gag tcc ctg gac cca cgg   3600
Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg
1185                1190                1195                1200

ccc ctg cgg cgg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg   3648
Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly
                1205                1210                1215

cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac   3696
Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His
            1220                1225                1230

cgt gag gat gca gcc gag ctt gac gac gac tcg gag gac agc tgc tgc   3744
Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys
        1235                1240                1245

ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag cgg tgc cgg   3792
Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg
    1250                1255                1260

agc agg agg cct ggg ccc tct acc ctc tac ctc ttc tcc cca cag aac   3840
Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn
1265                1270                1275                1280

cgg ttc cgc gtc tcc tgc cag aag gtc atc aca cac aag atg ttt gat   3888
Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp
                1285                1290                1295

cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc ctg   3936
His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu
            1300                1305                1310

gag agg cct gac att gat ccc ggc agc acc gag cgg gtc ttc ctc agc   3984
Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser
        1315                1320                1325

gtc tcc aat tac atc ttc acg gcc atc ttc gtg gcg gag atg atg gtg   4032
Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val
    1330                1335                1340

aag gtg gtg gcc ctg ggg ctg ctg tcc ggc gag cac gcc tac ctg cag   4080
Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Ala Tyr Leu Gln
1345                1350                1355                1360

agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg   4128
Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val
                1365                1370                1375

gac att gtc gtg gcc atg gcc tcg gct ggt ggc gcc aag atc ctg ggt   4176
Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly
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      1380                1385                1390

gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cct ctg agg gtc    4224
Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val
    1395                1400                1405

atc agc cgg gcc ccg ggc ctc aag ctg gtg gtg gag acg ctg ata tca    4272
Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser
1410                1415                1420

tca ctc agg ccc att ggg aac atc gtc ctc atc tgc tgc gcc ttc ttc    4320
Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe
1425                1430                1435                1440

atc att ttt ggc att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac    4368
Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr
            1445                1450                1455

tac tgc gag ggc ccc gac acc agg aac atc tcc acc aag gca cag tgc    4416
Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys
        1460                1465                1470

cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac    4464
Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn
    1475                1480                1485

ctg ggc cag gcc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat gga    4512
Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly
1490                1495                1500

tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac cag    4560
Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln
1505                1510                1515                1520

cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc    4608
Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser
            1525                1530                1535

ttc ctg ctc atc gtc agc ttc ttc gtg ctc aac atg ttc gtg ggc gtc    4656
Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val
        1540                1545                1550

gtg gtc gag aac ttc cac aag tgc cgg ccg cac cag gag gcg gag gag    4704
Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu
    1555                1560                1565

gcg cgg cgg cga gag gag aag cgg ctg cgg cgc cta gag agg agg cgc    4752
Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg
1570                1575                1580

agg agc act ttc ccc agc cca gag gcc cag cgc cgg ccc tac tat gcc    4800
Arg Ser Thr Phe Pro Ser Pro Glu Ala Gln Arg Arg Pro Tyr Tyr Ala
1585                1590                1595                1600

gac tac tcg ccc acg cgc cgc tgg att cac tcg ctg tgc acc agc cac    4848
Asp Tyr Ser Pro Thr Arg Arg Trp Ile His Ser Leu Cys Thr Ser His
            1605                1610                1615

tat ctc gac ctc ttc atc acc ttc atc atc tgt gtc aac gtc atc acc    4896
Tyr Leu Asp Leu Phe Ile Thr Phe Ile Ile Cys Val Asn Val Ile Thr
        1620                1625                1630

atg tcc atg gag cac tat aac caa ccc aag tcg ctg gac gag gcc ctc    4944
Met Ser Met Glu His Tyr Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu
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        1635                    1640                    1645

aag tac tgc aac tac gtc ttc acc atc gtg ttt gtc ttc gag gct gca    4992
Lys Tyr Cys Asn Tyr Val Phe Thr Ile Val Phe Val Phe Glu Ala Ala
    1650                    1655                    1660

ctg aag ctg gta gca ttt ggg ttc cgt cgg ttc ttc aag gac agg tgg    5040
Leu Lys Leu Val Ala Phe Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp
1665                    1670                    1675                1680

aac cag ctg gac ctg gcc atc gtg ctg ctg tca ctc atg ggc atc acg    5088
Asn Gln Leu Asp Leu Ala Ile Val Leu Leu Ser Leu Met Gly Ile Thr
                1685                    1690                    1695

ctg gag gag ata gag atg agc gcc gcg ctg ccc atc aac ccc acc atc    5136
Leu Glu Glu Ile Glu Met Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile
            1700                    1705                    1710

atc cgc atc atg cgc gtg ctt cgc att gcc cgt gtg ctg aag ctg ctg    5184
Ile Arg Ile Met Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu
        1715                    1720                    1725

aag atg gct acg ggc atg cgc gcc ctg ctg gac act gtg gtg caa gct    5232
Lys Met Ala Thr Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala
    1730                    1735                    1740

ctc ccc cag gtg ggg aac ctg ggc ctt ctt ttc atg ctc ctg ttt ttt    5280
Leu Pro Gln Val Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe
1745                    1750                    1755                1760

atc tat gct gcg ctg gga gtg gag ctg ttc ggg agg ctg gag tgc agt    5328
Ile Tyr Ala Ala Leu Gly Val Glu Leu Phe Gly Arg Leu Glu Cys Ser
                1765                    1770                    1775

gaa gac aac ccc tgc gag ggc ctg agc agg cac gcc acc ttc agc aac    5376
Glu Asp Asn Pro Cys Glu Gly Leu Ser Arg His Ala Thr Phe Ser Asn
            1780                    1785                    1790

ttc ggc atg gcc ttc ctc acg ctg ttc cgc gtg tcc acg ggg gac aac    5424
Phe Gly Met Ala Phe Leu Thr Leu Phe Arg Val Ser Thr Gly Asp Asn
        1795                    1800                    1805

tgg aac ggg atc atg aag gac acg ctg cgc gag tgc tcc cgt gag gac    5472
Trp Asn Gly Ile Met Lys Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp
    1810                    1815                    1820

aag cac tgc ctg agc tac ctg ccg gcc ccg tcg ccc gtc tac ttc gtg    5520
Lys His Cys Leu Ser Tyr Leu Pro Ala Pro Ser Pro Val Tyr Phe Val
1825                    1830                    1835                1840

acc ttc gtg ctg gtg ccc cag ttc gtg ctg gtg aac gtg gtg gtg gcc    5568
Thr Phe Val Leu Val Pro Gln Phe Val Leu Val Asn Val Val Val Ala
                1845                    1850                    1855

gtg ctc atg aag cac ctg gag gag agc aac aag gag gct cgg gag gat    5616
Val Leu Met Lys His Leu Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp
            1860                    1865                    1870

gcg gag ctg gac gcc gag atc gag ctg gag atg gcg cag ggc ccc ggg    5664
Ala Glu Leu Asp Ala Glu Ile Glu Leu Glu Met Ala Gln Gly Pro Gly
        1875                    1880                    1885

agt gca cgc cgg gtg gac gcg gac agg cct ccc ttg ccc cag gag agt    5712
Ser Ala Arg Arg Val Asp Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser
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1890 1895 1900

ccg ggc gcc agg gac gcc cca aac ctg gtt gca cgc aag gtg tcc gtg 5760
Pro Gly Ala Arg Asp Ala Pro Asn Leu Val Ala Arg Lys Val Ser Val
1905 1910 1915 1920

tcc agg atg ctc tcg ctg ccc aac gac agc tac atg ttc agg ccc gtg 5808
Ser Arg Met Leu Ser Leu Pro Asn Asp Ser Tyr Met Phe Arg Pro Val
1925 1930 1935

gtg cct gcc tcg gcg ccc cac ccc cgc ccg ctg cag gag gtg gag atg 5856
Val Pro Ala Ser Ala Pro His Pro Arg Pro Leu Gln Glu Val Glu Met
1940 1945 1950

gag acc tat ggg gcc ggc acc ccc ttg ggc tcc gtt gcc tct gtg cac 5904
Glu Thr Tyr Gly Ala Gly Thr Pro Leu Gly Ser Val Ala Ser Val His
1955 1960 1965

tct ccg ccc gca gag tcc tgt gcc tcc ctc cag atc cca ctg gct gtg 5952
Ser Pro Pro Ala Glu Ser Cys Ala Ser Leu Gln Ile Pro Leu Ala Val
1970 1975 1980

tcg tcc cca gcc agg agc ggc gag ccc ctc cac gcc ctg tcc cct cgg 6000
Ser Ser Pro Ala Arg Ser Gly Glu Pro Leu His Ala Leu Ser Pro Arg
1985 1990 1995 2000

ggc aca gcc cgc tcc ccc agt ctc agc cgg ctg ctc tgc aga cag gag 6048
Gly Thr Ala Arg Ser Pro Ser Leu Ser Arg Leu Leu Cys Arg Gln Glu
2005 2010 2015

gct gtg cac acc gat tcc ttg aag gga aga ttg aca gcc cta ggg aca 6096
Ala Val His Thr Asp Ser Leu Lys Gly Arg Leu Thr Ala Leu Gly Thr
2020 2025 2030

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2035 2040

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Arg Arg Pro Trp Pro Cys Gly Val Gly Gly Gly Val Pro Gly Glu Pro
20 25 30

cgg ggc gcc ggg acg cga ggc gga ggg ggg ttc gag ctc ggc gtg tca 144
Arg Gly Ala Gly Thr Arg Gly Gly Gly Gly Phe Glu Leu Gly Val Ser
35 40 45

ccc tcc gag agc ccg gcg gcc gag cgc tgc gcg gag ctg ggt gcc gac 192
Pro Ser Glu Ser Pro Ala Ala Glu Arg Cys Ala Glu Leu Gly Ala Asp
50 55 60

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gag gag cag cgc gtc ccg tac ccg gcc ttg gcg gcc acg gtc ttc ttc     240
Glu Glu Gln Arg Val Pro Tyr Pro Ala Leu Ala Ala Thr Val Phe Phe
 65                  70                  75                  80

tgc ctc ggt cag acc acg cgg ccg cgc agc tgg tgc ctc cgg ctg gtc     288
Cys Leu Gly Gln Thr Thr Arg Pro Arg Ser Trp Cys Leu Arg Leu Val
                 85                  90                  95

tgc aac cca tgg ttc gag cac gtg agc atg ctg gta atc atg ctc aac     336
Cys Asn Pro Trp Phe Glu His Val Ser Met Leu Val Ile Met Leu Asn
            100                 105                 110

tgc gtg acc ctg ggc atg ttc cgg ccc tgt gag gac gtt gag tgc ggc     384
Cys Val Thr Leu Gly Met Phe Arg Pro Cys Glu Asp Val Glu Cys Gly
        115                 120                 125

tcc gag cgc tgc aac atc ctg gag gcc ttt gac gcc ttc att ttc gcc     432
Ser Glu Arg Cys Asn Ile Leu Glu Ala Phe Asp Ala Phe Ile Phe Ala
    130                 135                 140

ttt ttt gcg gtg gag atg gtc atc aag atg gtg gcc ttg ggg ctg ttc     480
Phe Phe Ala Val Glu Met Val Ile Lys Met Val Ala Leu Gly Leu Phe
145                 150                 155                 160

ggg cag aag tgt tac ctg ggt gac acg tgg aac agg ctg gat ttc ttc     528
Gly Gln Lys Cys Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe
                165                 170                 175

atc gtc gtg gcg ggc atg atg gag tac tcg ttg gac gga cac aac gtg     576
Ile Val Val Ala Gly Met Met Glu Tyr Ser Leu Asp Gly His Asn Val
            180                 185                 190

agc ctc tcg gct atc agg acc gtg cgg gtg ctg cgg ccc ctc cgc gcc     624
Ser Leu Ser Ala Ile Arg Thr Val Arg Val Leu Arg Pro Leu Arg Ala
        195                 200                 205

atc aac cgc gtg cct agc atg cgg atc ctg gtc act ctg ctg ctg gat     672
Ile Asn Arg Val Pro Ser Met Arg Ile Leu Val Thr Leu Leu Leu Asp
    210                 215                 220

acg ctg ccc atg ctc ggg aac gtc ctt ctg ctg tgc ttc ttc gtc ttc     720
Thr Leu Pro Met Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe
225                 230                 235                 240

ttc att ttc ggc atc gtt ggc gtc cag ctc tgg gct ggc ctc ctg cgg     768
Phe Ile Phe Gly Ile Val Gly Val Gln Leu Trp Ala Gly Leu Leu Arg
                245                 250                 255

aac cgc tgc ttc ctg gac agt gcc ttt gtc agg aac aac aac ctg acc     816
Asn Arg Cys Phe Leu Asp Ser Ala Phe Val Arg Asn Asn Asn Leu Thr
            260                 265                 270

ttc ctg cgg ccg tac tac cag acg gag gag ggc gag gag aac ccg ttc     864
Phe Leu Arg Pro Tyr Tyr Gln Thr Glu Glu Gly Glu Glu Asn Pro Phe
        275                 280                 285

atc tgc tcc tca cgc cga gac aac ggc atg cag aag tgc tcg cac atc     912
Ile Cys Ser Ser Arg Arg Asp Asn Gly Met Gln Lys Cys Ser His Ile
    290                 295                 300

ccc ggc cgc cgc gac gtg cgc atg ccc tgc acc ctg ggc tgg gag gcc     960
Pro Gly Arg Arg Asp Val Arg Met Pro Cys Thr Leu Gly Trp Glu Ala
305                 310                 315                 320
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tac acg cag ccg cag gcc gag ggg gtg ggc gct gca cgc aac gcc tgc    1008
Tyr Thr Gln Pro Gln Ala Glu Gly Val Gly Ala Ala Arg Asn Ala Cys
                325                 330                 335

atc aac tgg aac cag tac tac aac gtg tgc cgc tcg ggc gac tcc aac    1056
Ile Asn Trp Asn Gln Tyr Tyr Asn Val Cys Arg Ser Gly Asp Ser Asn
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ccc cac aac ggt gcc atc aac ttc gac aac acc tgc tac gcc tgg atc    1104
Pro His Asn Gly Ala Ile Asn Phe Asp Asn Thr Cys Tyr Ala Trp Ile
        355                 360                 365

gcc atc ttc cag gtg atc acg ctg gaa ggc tgg gtg gac atc atg tac    1152
Ala Ile Phe Gln Val Ile Thr Leu Glu Gly Trp Val Asp Ile Met Tyr
    370                 375                 380

tac gtc atg gac gcc cac tca ttc tac aac ttc atc tac ttc atc ctg    1200
Tyr Val Met Asp Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu
385                 390                 395                 400

ctc atc atc gtg ggc tcc ttc ttc atg atc aac ctg tgc ctg gtg gtg    1248
Leu Ile Ile Val Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val
                405                 410                 415

att gcc acg cag ttc tcg gag acg aag cag cgg gag agt cag ctg atg    1296
Ile Ala Thr Gln Phe Ser Glu Thr Lys Gln Arg Glu Ser Gln Leu Met
            420                 425                 430

cgg gag cag cgg gca cgc cac ctg tcc aac gac agc acg ctg gcc agc    1344
Arg Glu Gln Arg Ala Arg His Leu Ser Asn Asp Ser Thr Leu Ala Ser
        435                 440                 445

ttc tcc gag cct ggc agc tgc tac gaa gag ctg ctg aag tac gtg ggc    1392
Phe Ser Glu Pro Gly Ser Cys Tyr Glu Glu Leu Leu Lys Tyr Val Gly
    450                 455                 460

cac ata ttc cgc aag gtc aag cgg cgc agc ttg cgc ctc tac gcc cgc    1440
His Ile Phe Arg Lys Val Lys Arg Arg Ser Leu Arg Leu Tyr Ala Arg
465                 470                 475                 480

tgg cag agc cgc tgg cgc aag aag gtg gac ccc agt gct gtg caa ggc    1488
Trp Gln Ser Arg Trp Arg Lys Lys Val Asp Pro Ser Ala Val Gln Gly
                485                 490                 495

cag ggt ccc ggg cac cgc cag cgc cgg gca ggc agg cac aca gcc tcg    1536
Gln Gly Pro Gly His Arg Gln Arg Arg Ala Gly Arg His Thr Ala Ser
            500                 505                 510

gtg cac cac ctg gtc tac cac cac cat cac cac cac cac cac cac tac    1584
Val His His Leu Val Tyr His His His His His His His His His Tyr
        515                 520                 525

cat ttc agc cat ggc agc ccc cgc agg ccc ggc ccc gag cca ggc gcc    1632
His Phe Ser His Gly Ser Pro Arg Arg Pro Gly Pro Glu Pro Gly Ala
    530                 535                 540

tgc gac acc agg ctg gtc cga gct ggc gcg ccc ccc tcg cca cct tcc    1680
Cys Asp Thr Arg Leu Val Arg Ala Gly Ala Pro Pro Ser Pro Pro Ser
545                 550                 555                 560

cca ggc cgc gga ccc ccc gac gca gag tct gtg cac agc atc tac cat    1728
Pro Gly Arg Gly Pro Pro Asp Ala Glu Ser Val His Ser Ile Tyr His
                565                 570                 575
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gcc gac tgc cac ata gag ggg ccg cag gag agg gcc cgg gtg ggc aca    1776
Ala Asp Cys His Ile Glu Gly Pro Gln Glu Arg Ala Arg Val Gly Thr
            580                 585                 590

tgc cgc agc cac tgc cgc tgc cag cct cag gct ggc cac agg gct ggg    1824
Cys Arg Ser His Cys Arg Cys Gln Pro Gln Ala Gly His Arg Ala Gly
        595                 600                 605

cac cat gaa cta ccc cac gat cct gcc ctc agg ggt ggg cag cgg caa    1872
His His Glu Leu Pro His Asp Pro Ala Leu Arg Gly Gly Gln Arg Gln
    610                 615                 620

agg cag cac cag ccc cgg acc caa ggg gaa gtg ggc cgg tgg acc gcc    1920
Arg Gln His Gln Pro Arg Thr Gln Gly Glu Val Gly Arg Trp Thr Ala
625                 630                 635                 640

agg cac cgg ggg cac ggc ccg ttg agc ttg aac agc cct gat ccc tac    1968
Arg His Arg Gly His Gly Pro Leu Ser Leu Asn Ser Pro Asp Pro Tyr
                645                 650                 655

gag aag atc ccg cat gtg gcc ggg gag cat gga ctg ggc caa gcc cct    2016
Glu Lys Ile Pro His Val Ala Gly Glu His Gly Leu Gly Gln Ala Pro
            660                 665                 670

ggc cat ctg tcg ggc ctc agt gtg ccc tgc ccc ctg ccc agc ccc cca    2064
Gly His Leu Ser Gly Leu Ser Val Pro Cys Pro Leu Pro Ser Pro Pro
        675                 680                 685

gcg ggc aca ctg acc tgt gag ctg aag agc tgc ccg tac tgc acc cgt    2112
Ala Gly Thr Leu Thr Cys Glu Leu Lys Ser Cys Pro Tyr Cys Thr Arg
    690                 695                 700

gcc ctg gag gac ccg gag ggt gag ctc agc ggc tcg gaa agt gga gac    2160
Ala Leu Glu Asp Pro Glu Gly Glu Leu Ser Gly Ser Glu Ser Gly Asp
705                 710                 715                 720

tca gat ggc cgt ggc gtc tat gaa ttc acg cag gac gtc cgg cac ggt    2208
Ser Asp Gly Arg Gly Val Tyr Glu Phe Thr Gln Asp Val Arg His Gly
                725                 730                 735

gac cgc tgg gac ccc acg cga cca ccc cgt gcg acg gac aca cca ggc    2256
Asp Arg Trp Asp Pro Thr Arg Pro Pro Arg Ala Thr Asp Thr Pro Gly
            740                 745                 750

cca ggc cca ggc agc ccc cag cgg cgg gca cag cag agg gca gcc ccg    2304
Pro Gly Pro Gly Ser Pro Gln Arg Arg Ala Gln Gln Arg Ala Ala Pro
        755                 760                 765

ggc gag cca ggc tgg atg ggc cgc ctc tgg gtt acc ttc agc ggc aag    2352
Gly Glu Pro Gly Trp Met Gly Arg Leu Trp Val Thr Phe Ser Gly Lys
    770                 775                 780

ctg cgc cgc atc gtg gac agc aag tac ttc agc cgt ggc atc atg atg    2400
Leu Arg Arg Ile Val Asp Ser Lys Tyr Phe Ser Arg Gly Ile Met Met
785                 790                 795                 800

gcc atc ctt gtc aac acg ctg agc atg ggc gtg gag tac cat gag cag    2448
Ala Ile Leu Val Asn Thr Leu Ser Met Gly Val Glu Tyr His Glu Gln
                805                 810                 815

ccc gag gag ctg act aat gct ctg gag atc agc aac atc gtg ttc acc    2496
Pro Glu Glu Leu Thr Asn Ala Leu Glu Ile Ser Asn Ile Val Phe Thr
            820                 825                 830
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agc atg ttt gcc ctg gag atg ctg ctg aag ctg ctg gcc tgc ggg cct    2544
Ser Met Phe Ala Leu Glu Met Leu Leu Lys Leu Leu Ala Cys Gly Pro
        835                 840                 845

ctg ggc tac atc cgg aac ccg tac aac atc ttc gac ggc atc atc gtg    2592
Leu Gly Tyr Ile Arg Asn Pro Tyr Asn Ile Phe Asp Gly Ile Ile Val
    850                 855                 860

gtc atc agc gtc tgg gag atc gtg ggg cag gcg gac ggt ggc ttg tct    2640
Val Ile Ser Val Trp Glu Ile Val Gly Gln Ala Asp Gly Gly Leu Ser
865                 870                 875                 880

gtg ctg cgc acc ttc cgg ctg ctg cgt gtg ctg aag ctg gtg cgc ttt    2688
Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu Lys Leu Val Arg Phe
                885                 890                 895

ctg cca gcc ctg cgg cgc cag ctc gtg gtg ctg gtg aag acc atg gac    2736
Leu Pro Ala Leu Arg Arg Gln Leu Val Val Leu Val Lys Thr Met Asp
            900                 905                 910

aac gtg gct acc ttc tgc acg ctg ctc atg ctc ttc att ttc atc ttc    2784
Asn Val Ala Thr Phe Cys Thr Leu Leu Met Leu Phe Ile Phe Ile Phe
        915                 920                 925

agc atc ctg ggc atg cac ctt ttc ggc tgc aag ttc agc ctg aag aca    2832
Ser Ile Leu Gly Met His Leu Phe Gly Cys Lys Phe Ser Leu Lys Thr
    930                 935                 940

gac acc gga gac acc gtg cct gac agg aag aac ttc gac tcc ctg ctg    2880
Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu
945                 950                 955                 960

tgg gcc atc gtc acc gtg ttc cag atc ctg acc cag gag gac tgg aac    2928
Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr Gln Glu Asp Trp Asn
                965                 970                 975

gtg gtc ctg tac aac ggc atg gcc tcc acc tcc tcc tgg gcc gcc ctc    2976
Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser Ser Trp Ala Ala Leu
            980                 985                 990

tac ttc gtg gcc ctc atg acc ttc ggc aac tat gtg ctc ttc aac ctg    3024
Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr Val Leu Phe Asn Leu
        995                 1000                1005

ctg gtg gcc atc ctc gtg gag ggc ttc cag gcg gag ggc gat gcc aac    3072
Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala Glu Gly Asp Ala Asn
    1010                1015                1020

aga tcc gac acg gac gag gac aag acg tcg gtc cac ttc gag gag gac    3120
Arg Ser Asp Thr Asp Glu Asp Lys Thr Ser Val His Phe Glu Glu Asp
1025                1030                1035                1040

ttc cac aag ctc aga gaa ctc cag acc aca gag ctg aag atg tgt tcc    3168
Phe His Lys Leu Arg Glu Leu Gln Thr Thr Glu Leu Lys Met Cys Ser
                1045                1050                1055

ctg gcc gtg acc ccc aac ggc acc tgg agg gac gag gca gcc tgt ccc    3216
Leu Ala Val Thr Pro Asn Gly Thr Trp Arg Asp Glu Ala Ala Cys Pro
            1060                1065                1070

ctc ccc tca tca tgt gca cag ctg cca cgc cca tgc cta ccc cca aga    3264
Leu Pro Ser Ser Cys Ala Gln Leu Pro Arg Pro Cys Leu Pro Pro Arg
        1075                1080                1085
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gct cac cat tcc tgg atg cag ccc cca gcc tcc cag act ctc ggc gtg 3312
Ala His His Ser Trp Met Gln Pro Pro Ala Ser Gln Thr Leu Gly Val
1090 1095 1100

gca gca gca gct ccg ggg acc cgc cac tgg gag acc aga agc ctc cgg 3360
Ala Ala Ala Ala Pro Gly Thr Arg His Trp Glu Thr Arg Ser Leu Arg
1105 1110 1115 1120

cag cct ccg aag ttc tcc ctg tgc ccc ctg ggg ccc agt ggc gcc tgg 3408
Gln Pro Pro Lys Phe Ser Leu Cys Pro Leu Gly Pro Ser Gly Ala Trp
1125 1130 1135

agc agc cgg cgc tcc agc tgg agc agc ctg ggc cgt gcc cag cct caa 3456
Ser Ser Arg Arg Ser Ser Trp Ser Ser Leu Gly Arg Ala Gln Pro Gln
1140 1145 1150

gcg ccg gcg tgc cag tgt ggg gaa cgt gag tcc ctg ctg tct ggc gag 3504
Ala Pro Ala Cys Gln Cys Gly Glu Arg Glu Ser Leu Leu Ser Gly Glu
1155 1160 1165

ggc aag ggc agc acc gac gac gaa gct gag gac ggc agg gcg cgc tcc 3552
Gly Lys Gly Ser Thr Asp Asp Glu Ala Glu Asp Gly Arg Ala Arg Ser
1170 1175 1180

ggg ccc cgt gcc acc cca ctg cgg cgg gcc gag tcc ctg gac cca cgg 3600
Gly Pro Arg Ala Thr Pro Leu Arg Arg Ala Glu Ser Leu Asp Pro Arg
1185 1190 1195 1200

ccc ctg cgg cgg ccg cct ccc gcc tac caa gtg cgc gat cgc gac ggg 3648
Pro Leu Arg Arg Pro Pro Pro Ala Tyr Gln Val Arg Asp Arg Asp Gly
1205 1210 1215

cag gtg gtg gcc ctg ccc agc gac ttc ttc ctg cgc atc gac agc cac 3696
Gln Val Val Ala Leu Pro Ser Asp Phe Phe Leu Arg Ile Asp Ser His
1220 1225 1230

cgt gag gat gca gcc gag ctt gac gac gac tcg gag gac agc tgc tgc 3744
Arg Glu Asp Ala Ala Glu Leu Asp Asp Asp Ser Glu Asp Ser Cys Cys
1235 1240 1245

ctc cgc ctg cat aaa gtg ctg gtg ccc tac aag ccc cag cgg tgc cgg 3792
Leu Arg Leu His Lys Val Leu Val Pro Tyr Lys Pro Gln Arg Cys Arg
1250 1255 1260

agc agg agg cct ggg ccc tct acc ctc tac ctc ttc tcc cca cag aac 3840
Ser Arg Arg Pro Gly Pro Ser Thr Leu Tyr Leu Phe Ser Pro Gln Asn
1265 1270 1275 1280

cgg ttc cgc gtc tcc tgc cag aag gtc atc aca cac aag atg ttt gat 3888
Arg Phe Arg Val Ser Cys Gln Lys Val Ile Thr His Lys Met Phe Asp
1285 1290 1295

cac gtg gtc ctc gtc ttc atc ttc ctc aac tgc gtc acc atc gcc ctg 3936
His Val Val Leu Val Phe Ile Phe Leu Asn Cys Val Thr Ile Ala Leu
1300 1305 1310

gag agg cct gac att gat ccc ggc agc acc gag cgg gtc ttc ctc agc 3984
Glu Arg Pro Asp Ile Asp Pro Gly Ser Thr Glu Arg Val Phe Leu Ser
1315 1320 1325

gtc tcc aat tac atc ttc acg gcc atc ttc gtg gcg gag atg atg gtg 4032
Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Ala Glu Met Met Val
1330 1335 1340

aag gtg gtg gcc ctg ggg ctg ctg tcc ggc gag cac gcc tac ctg cag 4080
Lys Val Val Ala Leu Gly Leu Leu Ser Gly Glu His Ala Tyr Leu Gln
1345 1350 1355 1360

agc agc tgg aac ctg ctg gat ggg ctg ctg gtg ctg gtg tcc ctg gtg 4128
Ser Ser Trp Asn Leu Leu Asp Gly Leu Leu Val Leu Val Ser Leu Val
1365 1370 1375

gac att gtc gtg gcc atg gcc tcg gct ggt ggc gcc aag atc ctg ggt 4176
Asp Ile Val Val Ala Met Ala Ser Ala Gly Gly Ala Lys Ile Leu Gly
1380 1385 1390

gtt ctg cgc gtg ctg cgt ctg ctg cgg acc ctg cgg cct ctg agg gtc 4224
Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu Arg Val
1395 1400 1405

atc agc cgg gcc ccg ggc ctc aag ctg gtg gtg gag acg ctg ata tca 4272
Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu Ile Ser
1410 1415 1420

tca ctc agg ccc att ggg aac atc gtc ctc atc tgc tgc gcc ttc ttc 4320
Ser Leu Arg Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala Phe Phe
1425 1430 1435 1440

atc att ttt ggc att ttg ggt gtg cag ctc ttc aaa ggg aag ttc tac 4368
Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys Phe Tyr
1445 1450 1455

tac tgc gag ggc ccc gac acc agg aac atc tcc acc aag gca cag tgc 4416
Tyr Cys Glu Gly Pro Asp Thr Arg Asn Ile Ser Thr Lys Ala Gln Cys
1460 1465 1470

cgg gcc gcc cac tac cgc tgg gtg cga cgc aag tac aac ttc gac aac 4464
Arg Ala Ala His Tyr Arg Trp Val Arg Arg Lys Tyr Asn Phe Asp Asn
1475 1480 1485

ctg ggc cag gcc ctg atg tcg ctg ttc gtg ctg tca tcc aag gat gga 4512
Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ser Ser Lys Asp Gly
1490 1495 1500

tgg gtg aac atc atg tac gac ggg ctg gat gcc gtg ggt gtc gac cag 4560
Trp Val Asn Ile Met Tyr Asp Gly Leu Asp Ala Val Gly Val Asp Gln
1505 1510 1515 1520

cag cct gtg cag aac cac aac ccc tgg atg ctg ctg tac ttc atc tcc 4608
Gln Pro Val Gln Asn His Asn Pro Trp Met Leu Leu Tyr Phe Ile Ser
1525 1530 1535

ttc ctg ctc atc gtc agc ttc ttc gtg ctc aac atg ttc gtg ggc gtc 4656
Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val Gly Val
1540 1545 1550

gtg gtc gag aac ttc cac aag tgc cgg ccg cac cag gag gcg gag gag 4704
Val Val Glu Asn Phe His Lys Cys Arg Pro His Gln Glu Ala Glu Glu
1555 1560 1565

gcg cgg cgg cga gag gag aag cgg ctg cgg cgc cta gag agg agg cgc 4752
Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Arg Arg Arg
1570 1575 1580

agg aag gcc cag cgc cgg ccc tac tat gcc gac tac tcg ccc acg cgc 4800
Arg Lys Ala Gln Arg Arg Pro Tyr Tyr Ala Asp Tyr Ser Pro Thr Arg
1585 1590 1595 1600

cgc tgg att cac tcg ctg tgc acc agc cac tat ctc gac ctc ttc atc 4848
Arg Trp Ile His Ser Leu Cys Thr Ser His Tyr Leu Asp Leu Phe Ile
1605 1610 1615

acc ttc atc atc tgt gtc aac gtc atc acc atg tcc atg gag cac tat 4896
Thr Phe Ile Ile Cys Val Asn Val Ile Thr Met Ser Met Glu His Tyr
1620 1625 1630

aac caa ccc aag tcg ctg gac gag gcc ctc aag tac tgc aac tac gtc 4944
Asn Gln Pro Lys Ser Leu Asp Glu Ala Leu Lys Tyr Cys Asn Tyr Val
1635 1640 1645

ttc acc atc gtg ttt gtc ttc gag gct gca ctg aag ctg gta gca ttt 4992
Phe Thr Ile Val Phe Val Phe Glu Ala Ala Leu Lys Leu Val Ala Phe
1650 1655 1660

ggg ttc cgt cgg ttc ttc aag gac agg tgg aac cag ctg gac ctg gcc 5040
Gly Phe Arg Arg Phe Phe Lys Asp Arg Trp Asn Gln Leu Asp Leu Ala
1665 1670 1675 1680

atc gtg ctg ctg tca ctc atg ggc atc acg ctg gag gag ata gag atg 5088
Ile Val Leu Leu Ser Leu Met Gly Ile Thr Leu Glu Glu Ile Glu Met
1685 1690 1695

agc gcc gcg ctg ccc atc aac ccc acc atc atc cgc atc atg cgc gtg 5136
Ser Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met Arg Val
1700 1705 1710

ctt cgc att gcc cgt gtg ctg aag ctg ctg aag atg gct acg ggc atg 5184
Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr Gly Met
1715 1720 1725

cgc gcc ctg ctg gac act gtg gtg caa gct ctc ccc cag gtg ggg aac 5232
Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val Gly Asn
1730 1735 1740

ctg ggc ctt ctt ttc atg ctc ctg ttt ttt atc tat gct gcg ctg gga 5280
Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala Leu Gly
1745 1750 1755 1760

gtg gag ctg ttc ggg agg ctg gag tgc agt gaa gac aac ccc tgc gag 5328
Val Glu Leu Phe Gly Arg Leu Glu Cys Ser Glu Asp Asn Pro Cys Glu
1765 1770 1775

ggc ctg agc agg cac gcc acc ttc agc aac ttc ggc atg gcc ttc ctc 5376
Gly Leu Ser Arg His Ala Thr Phe Ser Asn Phe Gly Met Ala Phe Leu
1780 1785 1790

acg ctg ttc cgc gtg tcc acg ggg gac aac tgg aac ggg atc atg aag 5424
Thr Leu Phe Arg Val Ser Thr Gly Asp Asn Trp Asn Gly Ile Met Lys
1795 1800 1805

gac acg ctg cgc gag tgc tcc cgt gag gac aag cac tgc ctg agc tac 5472
Asp Thr Leu Arg Glu Cys Ser Arg Glu Asp Lys His Cys Leu Ser Tyr
1810 1815 1820

ctg ccg gcc ccg tcg ccc gtc tac ttc gtg acc ttc gtg ctg gtg ccc 5520
Leu Pro Ala Pro Ser Pro Val Tyr Phe Val Thr Phe Val Leu Val Pro
1825 1830 1835 1840

cag ttc gtg ctg gtg aac gtg gtg gtg gcc gtg ctc atg aag cac ctg 5568
Gln Phe Val Leu Val Asn Val Val Val Ala Val Leu Met Lys His Leu
1845 1850 1855

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gag gag agc aac aag gag gct cgg gag gat gcg gag ctg gac gcc gag      5616
Glu Glu Ser Asn Lys Glu Ala Arg Glu Asp Ala Glu Leu Asp Ala Glu
            1860                1865                1870

atc gag ctg gag atg gcg cag ggc ccc ggg agt gca cgc cgg gtg gac      5664
Ile Glu Leu Glu Met Ala Gln Gly Pro Gly Ser Ala Arg Arg Val Asp
        1875                1880                1885

gcg gac agg cct ccc ttg ccc cag gag agt ccg ggc gcc agg gac gcc      5712
Ala Asp Arg Pro Pro Leu Pro Gln Glu Ser Pro Gly Ala Arg Asp Ala
    1890                1895                1900

cca aac ctg gtt gca cgc aag gtg tcc gtg tcc agg atg ctc tcg ctg      5760
Pro Asn Leu Val Ala Arg Lys Val Ser Val Ser Arg Met Leu Ser Leu
1905                1910                1915                1920

ccc aac gac agc tac atg ttc agg ccc gtg gtg cct gcc tcg gcg ccc      5808
Pro Asn Asp Ser Tyr Met Phe Arg Pro Val Val Pro Ala Ser Ala Pro
                1925                1930                1935

cac ccc cgc ccg ctg cag gag gtg gag atg gag acc tat ggg gcc ggc      5856
His Pro Arg Pro Leu Gln Glu Val Glu Met Glu Thr Tyr Gly Ala Gly
            1940                1945                1950

acc ccc ttg ggc tcc gct gcc tct gtg cac tct ccg ccc gca gag tcc      5904
Thr Pro Leu Gly Ser Val Ala Ser Val His Ser Pro Pro Ala Glu Ser
        1955                1960                1965

tgt gcc tcc ctc cag atc cca ctg gct gtg tcg tcc cca gcc agg agc      5952
Cys Ala Ser Leu Gln Ile Pro Leu Ala Val Ser Ser Pro Ala Arg Ser
    1970                1975                1980

ggc gag ccc ctc cac gcc ctg tcc cct cgg ggc aca gcc cgc tcc ccc      6000
Gly Glu Pro Leu His Ala Leu Ser Pro Arg Gly Thr Ala Arg Ser Pro
1985                1990                1995                2000

agt ctc agc cgg ctg ctc tgc aga cag gag gct gtg cac acc gat tcc      6048
Ser Leu Ser Arg Leu Leu Cys Arg Gln Glu Ala Val His Thr Asp Ser
                2005                2010                2015

ttg aag gga aga ttg aca gcc cta ggg aca ccc tgg atc ctg cag agc      6096
Leu Lys Gly Arg Leu Thr Ala Leu Gly Thr Pro Trp Ile Leu Gln Ser
            2020                2025                2030

ctg gtg aga aaa ccc cgg                                              6114
Leu Val Arg Lys Pro Arg
        2035


&lt;210&gt; 11
&lt;211&gt; 5469
&lt;212&gt; DNA
&lt;213&gt; Homo sapiens

&lt;220&gt;
&lt;221&gt; CDS
&lt;222&gt; (1)..(5469)

&lt;400&gt; 11
atg gct gag agc gcc tcc ccg ccc tcc tca tct gca gca gcc cca gcc      48
Met Ala Glu Ser Ala Ser Pro Pro Ser Ser Ser Ala Ala Ala Pro Ala
  1               5                  10                  15
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gct gag cca gga gtc acc acg gag cag ccc gga ccc cgg agc ccc cca    96
Ala Glu Pro Gly Val Thr Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro
            20                  25                  30

tcc tcc ccg cca ggc ctg gag gag cct ctg gat gga gct gat cct cat   144
Ser Ser Pro Pro Gly Leu Glu Glu Pro Leu Asp Gly Ala Asp Pro His
        35                  40                  45

gtc cca cac cca gac ctg gcg cct att gcc ttc ttc tgc ctg cga cag   192
Val Pro His Pro Asp Leu Ala Pro Ile Ala Phe Phe Cys Leu Arg Gln
    50                  55                  60

acc acc agc ccc cgg aac tgg tgc atc aag atg gtg tgc aac ccg tgg   240
Thr Thr Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp
65                  70                  75                  80

ttt gaa tgt gtc agc atg ctg gtg atc ctg ctg aac tgc gtg aca ctt   288
Phe Glu Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu
                85                  90                  95

ggc atg tac cag ccg tgc gac gac atg gac tgc ctg tcc gac cgc tgc   336
Gly Met Tyr Gln Pro Cys Asp Asp Met Asp Cys Leu Ser Asp Arg Cys
            100                 105                 110

aag atc atg cag gtc ttt gat gac ttc atc ttt atc ttc ttt gcc atg   384
Lys Ile Met Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met
        115                 120                 125

gag atg gtg ctc aag atg gtg gcc ctg ggg att ttt ggc aag aag tgc   432
Glu Met Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys
    130                 135                 140

tac ctc ggg gac aca tgg aac cgc ctg gat ttc ttc atc gtc atg gca   480
Tyr Leu Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala
145                 150                 155                 160

ggg atg gtc gag tac tcc ctg gac ctt cag aac atc aac ctg tca gcc   528
Gly Met Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala
                165                 170                 175

atc cgc acc gtg cgc gtc ctg agg ccc ctc aaa gcc atc aac cgc gtg   576
Ile Arg Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val
            180                 185                 190

ccc agt atg cgg atc ctg gtg aac ctg ctc ctg gac aca ctg ccc atg   624
Pro Ser Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met
        195                 200                 205

ctg ggg aat gtc ctg ctg ctc tgc ttc ttt gtc ttc ttc atc ttt ggc   672
Leu Gly Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly
    210                 215                 220

atc ata ggt gtg cag ctc tgg gcg ggc ctg ctg cgt aac cgc tgc ttc   720
Ile Ile Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe
225                 230                 235                 240

ctg gag gag aac ttc acc ata caa ggg gat gtg gcc ttg ccc cca tac   768
Leu Glu Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr
                245                 250                 255

tac cag ccg gag gag gat gat gag atg ccc ttc atc tgc tcc ctg tcg   816
Tyr Gln Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Ser
            260                 265                 270
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ggc gac aat ggg ata atg ggc tgc cat gag atc ccc ccg ctc aag gag     864
Gly Asp Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu
        275                 280                 285

cag ggc cgt gag tgc tgc ctg tcc aag gac gac gtc tac gac ttt ggg     912
Gln Gly Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly
    290                 295                 300

gcg ggg cgc cag gac ctc aat gcc agc ggc ctc tgt gtc aac tgg aac     960
Ala Gly Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn
305                 310                 315                 320

cgt tac tac aat gtg tgc cgc acg ggc agc gcc aac ccc cac aag ggt     1008
Arg Tyr Tyr Asn Val Cys Arg Thr Gly Ser Ala Asn Pro His Lys Gly
            325                 330                 335

gcc atc aac ttt gac aac atc ggt tat gct tgg att gtc atc ttc cag     1056
Ala Ile Asn Phe Asp Asn Ile Gly Tyr Ala Trp Ile Val Ile Phe Gln
        340                 345                 350

gtg atc act ctg gaa ggc tgg gtg gag atc atg tac tac gtg atg gat     1104
Val Ile Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp
    355                 360                 365

gct cac tcc ttc tac aac ttc atc tac ttc atc ctg ctt atc ata gtg     1152
Ala His Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val
370                 375                 380

ggc tcc ttc ttc atg atc aac ctg tgc ctc gtt gtc ata gcg acc cag     1200
Gly Ser Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln
385                 390                 395                 400

ttc tcg gag acc aag caa cgg gag cac cgg ctg atg ctg gag cag cgg     1248
Phe Ser Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu Glu Gln Arg
            405                 410                 415

cag cgc tac ctg tcc tcc agc acg gtg gcc agc tac gcc gag cct ggc     1296
Gln Arg Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu Pro Gly
        420                 425                 430

gac tgc tac gag gag atc ttc cag tat gtc tgc cac atc ctg cgc aag     1344
Asp Cys Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys
    435                 440                 445

gcc aag cgc cgc gcc ctg ggc ctc tac cag gcc ctg cag agc cgg cgc     1392
Ala Lys Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Ser Arg Arg
    450                 455                 460

cag gcc ctg ggc ccg gag gcc ccg gcc ccc gcc aaa cct ggg ccc cac     1440
Gln Ala Leu Gly Pro Glu Ala Pro Ala Pro Ala Lys Pro Gly Pro His
465                 470                 475                 480

gcc aag gag ccc cgg cac tac cag ctg tgc ccg caa cat agc ccc ctg     1488
Ala Lys Glu Pro Arg His Tyr Gln Leu Cys Pro Gln His Ser Pro Leu
            485                 490                 495

gat gcg acg ccc cac acc ctg gtg cag ccc atc ccc gcc acg ctg gct     1536
Asp Ala Thr Pro His Thr Leu Val Gln Pro Ile Pro Ala Thr Leu Ala
            500                 505                 510

tcc gat ccc gcc agc tgc cct tgc tgc cag cat gag gac ggc cgg cgg     1584
Ser Asp Pro Ala Ser Cys Pro Cys Cys Gln His Glu Asp Gly Arg Arg
        515                 520                 525
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ccc tcg ggc ctg ggc agc acc gac tcg ggc cag gag ggc tcg ggc tcc      1632
Pro Ser Gly Leu Gly Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser
    530                 535                 540

ggg agc tcc gct ggt ggc gag gac gag gcg gat ggg gac ggg gcc cgg      1680
Gly Ser Ser Ala Gly Gly Glu Asp Glu Ala Asp Gly Asp Gly Ala Arg
545                 550                 555                 560

agc agc gag gac gga gcc tcc tca gaa ctg ggg aag gag gag gag gag      1728
Ser Ser Glu Asp Gly Ala Ser Ser Glu Leu Gly Lys Glu Glu Glu Glu
                565                 570                 575

gag gag cag gcg gat ggg gcg gtc tgg ctg tgc ggg gat gtg tgg cgg      1776
Glu Glu Gln Ala Asp Gly Ala Val Trp Leu Cys Gly Asp Val Trp Arg
            580                 585                 590

gag acg cga gcc aag ctg cgc ggc atc gtg gac agc aag tac ttc aac      1824
Glu Thr Arg Ala Lys Leu Arg Gly Ile Val Asp Ser Lys Tyr Phe Asn
        595                 600                 605

cgg ggc atc atg atg gcc atc ctg gtc aac acc gtc agc atg ggc atc      1872
Arg Gly Ile Met Met Ala Ile Leu Val Asn Thr Val Ser Met Gly Ile
    610                 615                 620

gag cac cac gag cag ccg gag gag ctg acc aac atc ctg gag atc tgc      1920
Glu His His Glu Gln Pro Glu Glu Leu Thr Asn Ile Leu Glu Ile Cys
625                 630                 635                 640

aat gtg gtc ttc acc agc atg ttt gcc ctg gag atg atc ctg aag ctg      1968
Asn Val Val Phe Thr Ser Met Phe Ala Leu Glu Met Ile Leu Lys Leu
                645                 650                 655

gct gca ttt ggg ctc ttc gac tac ctg cgt aac ccc tac aac atc ttc      2016
Ala Ala Phe Gly Leu Phe Asp Tyr Leu Arg Asn Pro Tyr Asn Ile Phe
            660                 665                 670

gac agc atc att gtc atc atc agc atc tgg gag atc gtg ggg cag gcg      2064
Asp Ser Ile Ile Val Ile Ile Ser Ile Trp Glu Ile Val Gly Gln Ala
        675                 680                 685

gac ggt ggg ctg tcg gtg ctg cgg acc ttc cgg ctg ctg cgc gtg ctg      2112
Asp Gly Gly Leu Ser Val Leu Arg Thr Phe Arg Leu Leu Arg Val Leu
    690                 695                 700

aaa ctg gtg cgc ttc atg cct gcc ctg cgg cgc cag ctc gtg gtg ctc      2160
Lys Leu Val Arg Phe Met Pro Ala Leu Arg Arg Gln Leu Val Val Leu
705                 710                 715                 720

atg aag acc atg gac aac gtg gcc acc ttc tgc atg ctg ctc atg ctc      2208
Met Lys Thr Met Asp Asn Val Ala Thr Phe Cys Met Leu Leu Met Leu
                725                 730                 735

ttc atc ttc atc ttc agc atc ctt ggg atg cat att ttt ggc tgc aag      2256
Phe Ile Phe Ile Phe Ser Ile Leu Gly Met His Ile Phe Gly Cys Lys
            740                 745                 750

ttc agc ctc cgc acg gac act gga gac acg gtg ccc gac agg aag aac      2304
Phe Ser Leu Arg Thr Asp Thr Gly Asp Thr Val Pro Asp Arg Lys Asn
        755                 760                 765

ttc gac tcc ctg ctg tgg gcc atc gtc act gtg ttc cag atc ctc acc      2352
Phe Asp Ser Leu Leu Trp Ala Ile Val Thr Val Phe Gln Ile Leu Thr
    770                 775                 780
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cag gag gac tgg aac gtc gtt ctc tac aat ggc atg gcc tcc act tct 2400
Gln Glu Asp Trp Asn Val Val Leu Tyr Asn Gly Met Ala Ser Thr Ser
785 790 795 800

ccc tgg gcc tcc ctc tac ttt gtc gcc ctc atg acc ttc ggc aac tat 2448
Pro Trp Ala Ser Leu Tyr Phe Val Ala Leu Met Thr Phe Gly Asn Tyr
805 810 815

gtg ctc ttc aac ctg ctg gtg gcc atc ctg gtg gag ggc ttc cag gcg 2496
Val Leu Phe Asn Leu Leu Val Ala Ile Leu Val Glu Gly Phe Gln Ala
820 825 830

gag ggt gac gcc aat cgc tcc tac tcg gac gag gac cag agc tca tcc 2544
Glu Gly Asp Ala Asn Arg Ser Tyr Ser Asp Glu Asp Gln Ser Ser Ser
835 840 845

aac ata gaa gag ttt gat aag ctc cag gaa ggc ctg gac agc agc gga 2592
Asn Ile Glu Glu Phe Asp Lys Leu Gln Glu Gly Leu Asp Ser Ser Gly
850 855 860

gat ccc aag ctc tgc cca atc ccc atg acc ccc aat ggg cac ctg gac 2640
Asp Pro Lys Leu Cys Pro Ile Pro Met Thr Pro Asn Gly His Leu Asp
865 870 875 880

ccc agt ctc cca ctg ggt ggg cac cta ggt cct gct ggg gct gcg gga 2688
Pro Ser Leu Pro Leu Gly Gly His Leu Gly Pro Ala Gly Ala Ala Gly
885 890 895

cct gcc ccc cga ctc tca ctg cag ccg gac ccc atg ctg gtg gcc ctg 2736
Pro Ala Pro Arg Leu Ser Leu Gln Pro Asp Pro Met Leu Val Ala Leu
900 905 910

ggc tcc cga aag agc agc gtc atg tct cta ggg agg atg agc tat gac 2784
Gly Ser Arg Lys Ser Ser Val Met Ser Leu Gly Arg Met Ser Tyr Asp
915 920 925

cag cgc tcc ctg tcc agc tcc cgg agc tcc tac tac ggg cca tgg ggc 2832
Gln Arg Ser Leu Ser Ser Ser Arg Ser Ser Tyr Tyr Gly Pro Trp Gly
930 935 940

cgc agc gcg gcc tgg gcc agc cgt cgc tcc agc tgg aac agc ctc aag 2880
Arg Ser Ala Ala Trp Ala Ser Arg Arg Ser Ser Trp Asn Ser Leu Lys
945 950 955 960

cac aag ccg ccg tcg gcg gag cat gag tcc ctg ctc tct gcg gag cgc 2928
His Lys Pro Pro Ser Ala Glu His Glu Ser Leu Leu Ser Ala Glu Arg
965 970 975

ggc ggc ggc gcc cgg gtc tgc gag gtt gcc gcg gac gag ggg ccg ccg 2976
Gly Gly Gly Ala Arg Val Cys Glu Val Ala Ala Asp Glu Gly Pro Pro
980 985 990

cgg gcc gca ccc ctg cac acc cca cac gcc cac cac gtt cat cac ggg 3024
Arg Ala Ala Pro Leu His Thr Pro His Ala His His Val His His Gly
995 1000 1005

ccc cat ctg gcg cac cgc cac cgc cac cac cgc cgg acg ctg tcc ctc 3072
Pro His Leu Ala His Arg His Arg His His Arg Arg Thr Leu Ser Leu
1010 1015 1020

gac aac agg gac tcg gtg gac ctg gcc gag ctg gtg ccc gcg gtg ggc 3120
Asp Asn Arg Asp Ser Val Asp Leu Ala Glu Leu Val Pro Ala Val Gly
1025 1030 1035 1040

gcc cac ccc cgg gcc gcc tgg agg gcg gca ggc ccg gcc ccc ggg cat 3168
Ala His Pro Arg Ala Ala Trp Arg Ala Ala Gly Pro Ala Pro Gly His
1045 1050 1055

gag gac tgc aat ggc agg atg ccc agc atc gcc aaa gac gtc ttc acc 3216
Glu Asp Cys Asn Gly Arg Met Pro Ser Ile Ala Lys Asp Val Phe Thr
1060 1065 1070

aag atg ggc gac cgc ggg gat cgc ggg gag gat gag gag gaa atc gac 3264
Lys Met Gly Asp Arg Gly Asp Arg Gly Glu Asp Glu Glu Glu Ile Asp
1075 1080 1085

tac acc ctg tgc ttc cgc gtc cgc aag atg atc gac gtc tat aag ccc 3312
Tyr Thr Leu Cys Phe Arg Val Arg Lys Met Ile Asp Val Tyr Lys Pro
1090 1095 1100

gac tgg tgc gag gtc cgc gaa gac tgg tct gtc tac ctc ttc tct ccc 3360
Asp Trp Cys Glu Val Arg Glu Asp Trp Ser Val Tyr Leu Phe Ser Pro
1105 1110 1115 1120

gag aac agg ttc cgg gtc ctg tgt cag acc atc att gcc cac aaa ctc 3408
Glu Asn Arg Phe Arg Val Leu Cys Gln Thr Ile Ile Ala His Lys Leu
1125 1130 1135

ttc gac tac gtc gtc ctg gcc ttc atc ttt ctc aac tgc atc acc atc 3456
Phe Asp Tyr Val Val Leu Ala Phe Ile Phe Leu Asn Cys Ile Thr Ile
1140 1145 1150

gcc ctg gag cgg cct cag atc gag gcc ggc agc acc gaa cgc atc ttt 3504
Ala Leu Glu Arg Pro Gln Ile Glu Ala Gly Ser Thr Glu Arg Ile Phe
1155 1160 1165

ctc acc gtg tcc aac tac atc ttc acg gcc atc ttc gtg ggc gag atg 3552
Leu Thr Val Ser Asn Tyr Ile Phe Thr Ala Ile Phe Val Gly Glu Met
1170 1175 1180

aca ttg aag gta gtc tcg ctg ggc ctg tac ttc ggc gag cag gcg tac 3600
Thr Leu Lys Val Val Ser Leu Gly Leu Tyr Phe Gly Glu Gln Ala Tyr
1185 1190 1195 1200

cta cgc agc agc tgg aac gtg ctg gat ggc ttt ctt gtc ttc gtg tcc 3648
Leu Arg Ser Ser Trp Asn Val Leu Asp Gly Phe Leu Val Phe Val Ser
1205 1210 1215

atc atc gac atc gtg gtg tcc ctg gcc tca gcc ggg gga gcc aag atc 3696
Ile Ile Asp Ile Val Val Ser Leu Ala Ser Ala Gly Gly Ala Lys Ile
1220 1225 1230

ttg ggg gtc ctc cga gtc ttg cgg ctc ctg cgc acc cta cgc ccc ctg 3744
Leu Gly Val Leu Arg Val Leu Arg Leu Leu Arg Thr Leu Arg Pro Leu
1235 1240 1245

cgt gtc atc agc cgg gcg ccg ggc ctg aag ctg gtg gtg gag aca ctc 3792
Arg Val Ile Ser Arg Ala Pro Gly Leu Lys Leu Val Val Glu Thr Leu
1250 1255 1260

atc tcc tcc ctc aag ccc atc ggc aac atc gtg ctc atc tgc tgt gcc 3840
Ile Ser Ser Leu Lys Pro Ile Gly Asn Ile Val Leu Ile Cys Cys Ala
1265 1270 1275 1280

ttc ttc atc atc ttt ggc atc ctg gga gtg cag ctc ttc aag ggc aag 3888
Phe Phe Ile Ile Phe Gly Ile Leu Gly Val Gln Leu Phe Lys Gly Lys
1285 1290 1295

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ttc tac cac tgt ctg ggc gtg gac acc cgc aac atc acc aac cgc tcg     3936
Phe Tyr His Cys Leu Gly Val Asp Thr Arg Asn Ile Thr Asn Arg Ser
            1300                1305                1310

gac tgc atg gcc gcc aac tac cgc tgg gtc cat cac aaa tac aac ttc     3984
Asp Cys Met Ala Ala Asn Tyr Arg Trp Val His His Lys Tyr Asn Phe
        1315                1320                1325

gac aac ctg ggc cag gct ctg atg tcc ctc ttt gtc ctg gca tcc aag     4032
Asp Asn Leu Gly Gln Ala Leu Met Ser Leu Phe Val Leu Ala Ser Lys
    1330                1335                1340

gat ggt tgg gtg aac atc atg tac aat gga ctg gat gct gtt gct gtg     4080
Asp Gly Trp Val Asn Ile Met Tyr Asn Gly Leu Asp Ala Val Ala Val
1345                1350                1355                1360

gac cag cag cct gtg acc aac cac aac ccc tgg atg ctg ctg tac ttc     4128
Asp Gln Gln Pro Val Thr Asn His Asn Pro Trp Met Leu Leu Tyr Phe
                1365                1370                1375

atc tcc ttc ctg ctc atc gtc agc ttc ttt gtg ctc aac atg ttt gtg     4176
Ile Ser Phe Leu Leu Ile Val Ser Phe Phe Val Leu Asn Met Phe Val
            1380                1385                1390

ggt gtc gtg gtg gag aac ttc cac aag tgc cgg cag cac cag gag gct     4224
Gly Val Val Val Glu Asn Phe His Lys Cys Arg Gln His Gln Glu Ala
        1395                1400                1405

gaa gag gca cgg cgg cgt gag gag aag cgg ctg cgg cgc ctg gag aag     4272
Glu Glu Ala Arg Arg Arg Glu Glu Lys Arg Leu Arg Arg Leu Glu Lys
    1410                1415                1420

aag cgc cgg aag gcc cag cgg ctg ccc tac tat gcc acc tat tgt cac     4320
Lys Arg Arg Lys Ala Gln Arg Leu Pro Tyr Tyr Ala Thr Tyr Cys His
1425                1430                1435                1440

acc cgg ctg ctc atc cac tcc atg tgc acc agc cac tac ctg gac atc     4368
Thr Arg Leu Leu Ile His Ser Met Cys Thr Ser His Tyr Leu Asp Ile
                1445                1450                1455

ttc atc acc ttc atc atc tgc ctc aac gtg gtc acc atg tcc ctg gag     4416
Phe Ile Thr Phe Ile Ile Cys Leu Asn Val Val Thr Met Ser Leu Glu
            1460                1465                1470

cac tac aat cag ccc acg tcc ctg gag aca gcc ctc aag tac tgc aac     4464
His Tyr Asn Gln Pro Thr Ser Leu Glu Thr Ala Leu Lys Tyr Cys Asn
        1475                1480                1485

tat atg ttc acc act gtc ttt gtg ctg gag gct gtg ctg aag ctg gtg     4512
Tyr Met Phe Thr Thr Val Phe Val Leu Glu Ala Val Leu Lys Leu Val
    1490                1495                1500

gca ttt ggt ctg agg cgc tta ttc aag gac cga tgg aac cag ctg gac     4560
Ala Phe Gly Leu Arg Arg Leu Phe Lys Asp Arg Trp Asn Gln Leu Asp
1505                1510                1515                1520

ctg gcc att gtg cta ctg tca gtc atg ggc atc acc ctg gag gag atc     4608
Leu Ala Ile Val Leu Leu Ser Val Met Gly Ile Thr Leu Glu Glu Ile
                1525                1530                1535

gag atc aat gcg gcc ctg ccc atc aat ccc acc atc atc cgc atc atg     4656
Glu Ile Asn Ala Ala Leu Pro Ile Asn Pro Thr Ile Ile Arg Ile Met
            1540                1545                1550
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agg gtt ctg cgc att gcc cga gtg ctg aag ctg ttg aag atg gcc aca    4704
Arg Val Leu Arg Ile Ala Arg Val Leu Lys Leu Leu Lys Met Ala Thr
            1555                1560                1565

gga atg cgg gcc ctg ctg gac acg gtg gtg caa gct ttg ccc cag gtg    4752
Gly Met Arg Ala Leu Leu Asp Thr Val Val Gln Ala Leu Pro Gln Val
        1570                1575                1580

ggc aac ctg ggc ctc ctc ttc atg ctg ctc ttc ttc atc tat gct gct    4800
Gly Asn Leu Gly Leu Leu Phe Met Leu Leu Phe Phe Ile Tyr Ala Ala
1585                1590                1595                1600

ctc ggg gtg gag ctc ttt ggg aag ctg gtc tgc aac gac gag aac ccg    4848
Leu Gly Val Glu Leu Phe Gly Lys Leu Val Cys Asn Asp Glu Asn Pro
                1605                1610                1615

tgc gag ggc atg agc cgg cat gcc acc ttc gag aac ttc ggc atg gcc    4896
Cys Glu Gly Met Ser Arg His Ala Thr Phe Glu Asn Phe Gly Met Ala
            1620                1625                1630

ttc ctc aca ctc ttc cag gtc tcc acg ggt gac aac tgg aac ggg atc    4944
Phe Leu Thr Leu Phe Gln Val Ser Thr Gly Asp Asn Trp Asn Gly Ile
        1635                1640                1645

atg aag gac acg ctg cgg gac tgc acc cac gac gag cgc agc tgc ctg    4992
Met Lys Asp Thr Leu Arg Asp Cys Thr His Asp Glu Arg Ser Cys Leu
    1650                1655                1660

agc agc ctg cag ttt gtg tcg ccg ctg tac ttc gtg agc ttc gtg ctc    5040
Ser Ser Leu Gln Phe Val Ser Pro Leu Tyr Phe Val Ser Phe Val Leu
1665                1670                1675                1680

acc gcg cag ttc gtg ctc atc aac gtg gtg gtg gct gtg ctc atg aag    5088
Thr Ala Gln Phe Val Leu Ile Asn Val Val Val Ala Val Leu Met Lys
                1685                1690                1695

cac ctg gac gac agc aac aag gag gcg cag gag gac gcc gag atg gat    5136
His Leu Asp Asp Ser Asn Lys Glu Ala Gln Glu Asp Ala Glu Met Asp
            1700                1705                1710

gcc gag ctc gag ctg gag atg gcc cat ggc ctg ggc cct ggc ccg agg    5184
Ala Glu Leu Glu Leu Glu Met Ala His Gly Leu Gly Pro Gly Pro Arg
        1715                1720                1725

ctg cct acc ggc tcc ccg ggc gcc cct ggc cga ggg ccg gga ggg gcg    5232
Leu Pro Thr Gly Ser Pro Gly Ala Pro Gly Arg Gly Pro Gly Gly Ala
    1730                1735                1740

ggc ggc ggg ggc gac acc gat ggc ggc ttg tgc cgg cgc tgc tac tcg    5280
Gly Gly Gly Gly Asp Thr Asp Gly Gly Leu Cys Arg Arg Cys Tyr Ser
1745                1750                1755                1760

cct gcc cag gag aac ctg tgg ctg gac agc gtc tct tta atc atc aag    5328
Pro Ala Gln Glu Asn Leu Trp Leu Asp Ser Val Ser Leu Ile Ile Lys
                1765                1770                1775

gac tcc ttg gag ggg gag ctg acc atc atc gac aac ctg tcg ggc tcc    5376
Asp Ser Leu Glu Gly Glu Leu Thr Ile Ile Asp Asn Leu Ser Gly Ser
            1780                1785                1790

atc ttc cac cac tac tcc tcg cct gcc ggc tgc aag aag tgt cac cac    5424
Ile Phe His His Tyr Ser Ser Pro Ala Gly Cys Lys Lys Cys His His
        1795                1800                1805
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gac aag caa gag aca ggt cct cgt cca tcc tgc tgg gtg acg acc 5469
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1810 1815 1820

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gag ccg gga atc act gag cag ccg ggg ccc cgg agt ccc cct cca tcc 96
Glu Pro Gly Ile Thr Glu Gln Pro Gly Pro Arg Ser Pro Pro Pro Ser
20 25 30

cct cca ggc ctg gag gag cca ttg gaa gga acc aac cct gac gtc cca 144
Pro Pro Gly Leu Glu Glu Pro Leu Glu Gly Thr Asn Pro Asp Val Pro
35 40 45

cat cca gac ctg gct cct gtt gct ttc ttc tgc ctg cgc cag acc acg 192
His Pro Asp Leu Ala Pro Val Ala Phe Phe Cys Leu Arg Gln Thr Thr
50 55 60

agc cca cgg aac tgg tgc atc aag atg gtt tgt aac ccg tgg ttc gag 240
Ser Pro Arg Asn Trp Cys Ile Lys Met Val Cys Asn Pro Trp Phe Glu
65 70 75 80

tgt gtg agc atg ctg gtt att ctg ctg aac tgt gtg acc ctg ggc atg 288
Cys Val Ser Met Leu Val Ile Leu Leu Asn Cys Val Thr Leu Gly Met
85 90 95

tac cag cca tgt gat gac atg gag tgc ctg tcg gac cgt tgc aag atc 336
Tyr Gln Pro Cys Asp Asp Met Glu Cys Leu Ser Asp Arg Cys Lys Ile
100 105 110

ctg cag gtc ttc gat gac ttc atc ttc atc ttc ttt gcc atg gag atg 384
Leu Gln Val Phe Asp Asp Phe Ile Phe Ile Phe Phe Ala Met Glu Met
115 120 125

gtg ctt aag atg gtg gcc ctg ggc att ttt ggc aag aag tgc tac ctc 432
Val Leu Lys Met Val Ala Leu Gly Ile Phe Gly Lys Lys Cys Tyr Leu
130 135 140

gga gac aca tgg aac cgc ctg gat ttc ttc att gtc atg gca ggg atg 480
Gly Asp Thr Trp Asn Arg Leu Asp Phe Phe Ile Val Met Ala Gly Met
145 150 155 160

gtt gag tac tct ctg gac cta cag aac atc aac ctg tca gcc atc cgc 528
Val Glu Tyr Ser Leu Asp Leu Gln Asn Ile Asn Leu Ser Ala Ile Arg
165 170 175

act gtg cgt gtc ctg agg cct ctc aaa gcc atc aac cgt gta ccc agc 576
Thr Val Arg Val Leu Arg Pro Leu Lys Ala Ile Asn Arg Val Pro Ser
180 185 190

atg cgg atc ctg gtg aac ctg ctg ctc gac acg ctg ccc atg ctg ggg 624

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Met Arg Ile Leu Val Asn Leu Leu Leu Asp Thr Leu Pro Met Leu Gly
        195                 200                     205

aac gtg ctc ctg ctc tgt ttc ttc gtc ttc ttc atc ttc ggc atc att     672
Asn Val Leu Leu Leu Cys Phe Phe Val Phe Phe Ile Phe Gly Ile Ile
    210                 215                     220

ggc gtg cag ctc tgg gca ggc ctg cta cgg aac cgc tgc ttc ctg gaa     720
Gly Val Gln Leu Trp Ala Gly Leu Leu Arg Asn Arg Cys Phe Leu Glu
225                 230                     235                 240

gag aac ttc acc ata caa ggg gat gtg gcc ctg ccc cct tat tac caa     768
Glu Asn Phe Thr Ile Gln Gly Asp Val Ala Leu Pro Pro Tyr Tyr Gln
                245                     250                 255

cca gag gag gat gac gag atg ccc ttt atc tgc tcc ctg act ggg gac     816
Pro Glu Glu Asp Asp Glu Met Pro Phe Ile Cys Ser Leu Thr Gly Asp
            260                 265                     270

aat ggc atc atg ggc tgc cac gag atc ccc cca ctg aag gag cag ggc     864
Asn Gly Ile Met Gly Cys His Glu Ile Pro Pro Leu Lys Glu Gln Gly
        275                 280                     285

cgg gaa tgc tgc ctg tcc aaa gat gat gtg tat gac ttc ggg gcg ggg     912
Arg Glu Cys Cys Leu Ser Lys Asp Asp Val Tyr Asp Phe Gly Ala Gly
    290                 295                 300

cgc cag gac ctc aac gcc agc ggt ctg tgc gtc aac tgg aac cgc tac     960
Arg Gln Asp Leu Asn Ala Ser Gly Leu Cys Val Asn Trp Asn Arg Tyr
305                 310                     315                 320

tac aac gtc tgc cgc acg ggc aac gcc aac cct cac aag ggc gcc atc     1008
Tyr Asn Val Cys Arg Thr Gly Asn Ala Asn Pro His Lys Gly Ala Ile
                325                     330                 335

aac ttt gac aac att ggc tat gcc ggg att gtg att ttc cag gtg atc     1056
Asn Phe Asp Asn Ile Gly Tyr Ala Gly Ile Val Ile Phe Gln Val Ile
            340                 345                     350

act ctg gaa ggc tgg gtg gag atc atg tac tat gtg atg gac gca cat     1104
Thr Leu Glu Gly Trp Val Glu Ile Met Tyr Tyr Val Met Asp Ala His
        355                 360                     365

tct ttc tac aac ttc atc tac ttc att ctg ctc atc ata gtg ggc tcc     1152
Ser Phe Tyr Asn Phe Ile Tyr Phe Ile Leu Leu Ile Ile Val Gly Ser
    370                 375                     380

ttc ttc atg atc aac ttg tgc ctc gtt gtc ata gca acc cag ttc tct     1200
Phe Phe Met Ile Asn Leu Cys Leu Val Val Ile Ala Thr Gln Phe Ser
385                 390                     395                 400

gag acc aag caa cgg gag cac cgg ctg atg ctg gag caa cgc cag cgc     1248
Glu Thr Lys Gln Arg Glu His Arg Leu Met Leu Glu Gln Arg Gln Arg
                405                     410                 415

tac ctg tcc tcc agc acg gtg gcc agt tac gct gag ccc ggt gat tgc     1296
Tyr Leu Ser Ser Ser Thr Val Ala Ser Tyr Ala Glu Pro Gly Asp Cys
            420                 425                     430

tat gag gag atc ttc caa tat gtc tgt cac atc ctt cgc aaa gcc aag     1344
Tyr Glu Glu Ile Phe Gln Tyr Val Cys His Ile Leu Arg Lys Ala Lys
        435                 440                     445

cgc cgt gcc cta ggc ctc tac cag gcc ctg cag aac cgg cgc cag gcc     1392
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Arg Arg Ala Leu Gly Leu Tyr Gln Ala Leu Gln Asn Arg Arg Gln Ala
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465                 470                 475                 480

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Glu Pro Ser His Cys Lys Leu Cys Pro Arg His Ser Pro Leu Asp Pro
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act ccc cac aca ctg gtg cag ccc atc tct gcc att ctg gcc tct gac      1536
Thr Pro His Thr Leu Val Gln Pro Ile Ser Ala Ile Leu Ala Ser Asp
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Pro Ser Ser Cys Pro His Cys Gln His Glu Ala Gly Arg Arg Pro Ser
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Gly Leu Gly Ser Thr Asp Ser Gly Gln Glu Gly Ser Gly Ser Gly Gly
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tct gca gag gcc gaa gcc aat ggg gat gga ctc cag agc agt gag gat      1680
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Gly Val Ser Ser Asp Leu Gly Lys Glu Glu Glu Gln Glu Asp Gly Ala
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gcc cga ctg tgt ggg gat gtg tgg cgc gag aca cga aaa aag ctg cgg      1776
Ala Arg Leu Cys Gly Asp Val Trp Arg Glu Thr Arg Lys Lys Leu Arg
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Gly Ile Val Asp Ser Lys Tyr Phe Asn Arg Gly Ile Met Met Ala Ile
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ctg gtg aac aca gtc agc atg ggc atc gag cac cac gaa cag ccc gag      1872
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ttt gcc ctg gag atg atc ctg aaa ctg gcc gcc ttt ggg ctc ttc gac      1968
Phe Ala Leu Glu Met Ile Leu Lys Leu Ala Ala Phe Gly Leu Phe Asp
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Tyr Leu Arg Asn Pro Tyr Asn Ile Phe Asp Ser Ile Ile Val Ile Ile
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Ala Thr Phe Cys Met Leu Leu Met Leu Phe Ile Phe Ile Phe Ser Ile
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Gly Asp Thr Val Pro Asp Arg Lys Asn Phe Asp Ser Leu Leu Trp Ala
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Cys Ser Asp Glu Asp Gln Ser Ser Ser Asn Leu Glu Glu Phe Asp Lys
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Pro Met Thr Pro Asn Gly His Leu Asp Pro Ser Leu Pro Leu Gly Ala
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cat ctg ggt cct gct ggt acc atg ggt act gcc ccc cgc ctc tca ctg      2688
His Leu Gly Pro Ala Gly Thr Met Gly Thr Ala Pro Arg Leu Ser Leu
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cag cca gac ccg gta ctg gtg gcc cta gac tct cgg aaa agc agt gtc      2736
Gln Pro Asp Pro Val Leu Val Ala Leu Asp Ser Arg Lys Ser Ser Val
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Arg Ser Ser Tyr Tyr Gly Pro Trp Gly Arg Ser Gly Thr Trp Ala Ser
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995 1000 1005

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Trp Arg Gly Ala Gly Gln Ala Pro Gly His Glu Asp Cys Asn Gly Arg
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Met Pro Asn Ile Ala Lys Asp Val Phe Thr Lys Met Asp Asp Arg Arg
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<213> Homo sapiens

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1 5 10 15

Lys Met Ala

INTERNATIONAL SEARCH REPORT

International Application No
PCT/US 98/23161

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 C12N15/12 C07K14/705 C07K16/28 C12N5/10 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 04144 A (NEUREX CORP) 9 February 1995	1,2,7, 10-18, 20-22
Y	see abstract; claims 1-10	3,19

X	NOONEY JM (REPRINT) ET AL: "Identifying neuronal non-L Ca2+ channels - more than stamp collecting?" TRENDS IN PHARMACOLOGICAL SCIENCES, 10-1997, 18, 363-371, XP002093637 see page 369, right-hand column - page 370, right-hand column	1,2, 10-16, 20-22

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[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
16 February 1999	09/03/1999

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Gurdjian, D

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Form PCT/ISA/210 (second sheet) (July 1992)

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication,where appropriate, of the relevant passages	Relevant to claim No.
X	ERTEL S I ET AL: "Low-voltage-activated T-type Cachannels" TRENDS IN PHARMACOLOGICAL SCIENCES, vol. 18, no. 2, February 1997, page 37-42 XP004055849 see page 39, left-hand column, paragraph 4 - page 40, middle column, paragraph 1; table 1 ---	1,2, 10-16, 20-22
X	DZHURA IO ET AL: "Characterization of hypothalamic low-voltage-activated Ca channels based on their functional expression in Xenopus oocytes." NEUROSCIENCE, FEB 1996, 70 (3) P729-38, XP002093638 UNITED STATES see the whole document ---	1,2, 10-18, 20-22
Y	WILSON R ET AL: "2.2 MB OF CONTIGUOUS NUCLEOTIDE SEQUENCE FROM CHROMOSOME III OF C ELEGANS" NATURE, vol. 368, 3 March 1994, pages 32-38, XP002910426 see abstract	3,19
Y	& EMBL DATABASE Accession number q18840 WILSON R. ET AL. 1996 see the whole document ---	3,19
A	WO 93 04083 A (SALK INST BIOTECH IND) 4 March 1993 see abstract; claims 1-39 ---	1-22
P,X	PEREZ-REYES E ET AL: "Molecular characterization of a neuronal low-voltage-activated T-type calcium channel 'see comments!" NATURE, FEB 26 1998, 391 (6670) P896-900, XP002093639 ENGLAND see the whole document ---	1-15, 20-22
P,X	CRIBBS LL ET AL: "Cloning and characterization of alpha1H from human heart, a member of the T-type Ca2+ channel gene family." CIRC RES, JUL 13 1998, 83 (1) P103-9, XP002093640 UNITED STATES see the whole document -----	1-22

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INTERNATIONAL SEARCH REPORT

Information on patent family members

Interr ıal Application No

PCT/US 98/23161

Patent document cited in search report		Publication date	Patent family member(s)			Publication date
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			JP	9501051	T	04-02-1997
WO 9304083	A	04-03-1993	US	5429921	A	04-07-1995
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